

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 18, 2005, 06:59:55 ; Search time 2319 Seconds

(without alignments)  
9319.114 Million cell updates/sec

Title: US-09-763-019-5

Perfect score: 446

Sequence: 1 atgtgaaatcggtcggtgc.....ttccaaaacgttgaaacatccg 446

Scoring table: IDENTITY\_NUC Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Database : GenEtbl:\*

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2: 9b_htg*:*
3: 9b_in:*
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6: 9b_pat:*
7: 9b_ph:*
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12: 9b_sy:*
13: 9b_un:*
14: 9b_y1:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Description	Length	DB ID
1	446	100.0	BD22332 Method of Polynucleotide	446	6
2	446	100.0	BD22332 Method of Polynucleotide	446	6
3	287.2	64.4	BD22332 Method of Polynucleotide	606	6
4	284	63.7	BD22332 Method of Polynucleotide	557	6
5	215.2	48.3	BD22332 Method of Polynucleotide	534	6
6	215.2	48.3	BD22332 Method of Polynucleotide	534	6
7	212	47.5	BD22332 Method of Polynucleotide	485	6
8	177.2	39.7	BD22332 Method of Polynucleotide	577	6
9	173.2	38.8	BD22332 Method of Polynucleotide	485	6
10	172.2	38.6	BD22332 Method of Polynucleotide	446	6
11	170	38.1	BD22332 Method of Polynucleotide	1093	6
12	169.2	37.9	BD22332 Method of Polynucleotide	522	6
13	168.6	37.8	BD22332 Method of Polynucleotide	460	6
14	168.6	37.8	BD22332 Method of Polynucleotide	503	6
15	167.2	37.5	BD22332 Method of Polynucleotide	534	6
16	166	37.2	BD22332 Method of Polynucleotide	434	6
17	166	37.2	BD22332 Method of Polynucleotide	437	6
18	166	37.2	BD22332 Method of Polynucleotide	443	6
19	166	37.2	BD22332 Method of Polynucleotide	488	6

RESULT	1	BD22332	446 bp DNA linear	PAT 17-JUL-2003
LOCUS			Method of genetic expression of polyprotein in plant.	
DEFINITION				
ACCESSION		BD22332		
KEYWORD		BD22332-1 GI:33033002		
SOURCE		Dahlia merckii (bedding dahlia)		
ORGANISM		Dahlia merckii		
		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; campanulids; Asterales; Asteraceae; Asteroidae; Coreopsidae; Dahlia.		
REFERENCE		1 (bases 1 to 446)		
AUTHORS		Broekaert,W.F., Francois,I.E.J.A., Boile,M.F.C.D., Evans,I.J. and Ray,J.A.		
TITLE		Method of genetic expression of polyprotein in plant		
JOURNAL		SYNGETA LTD		
COMMENT		OS Dahlia merckii		
		PN JPP 200223047-A/1		
		PD 30-JUL-2002		
		PP 17-AUG-1999 JP 20000566429		
		PR 18-AUG-1998 GB 9818001,1,04-DEC-1998 GB		9826753.7 PI
		PC C12N5/09,A01H1/00,C07K1/12,C12N5/10,C12P21/02/(C12N5/10, PC C12R1:1), MIGUEL FRANCISCO COLETA DE BOILE,IAN JEFFREY EVANS,JOHN PI ANTHONY RAY WILLEM FRANS BROEKERT,ISABELLE ELSA JEANNE AUGUSTINE FRANCOIS,		
		PC C12N5/00,C12N5/00,(C12N5/00,C12R1:91) Location/Qualifiers		
		CC Method of genetic expression of polyprotein in plant PH Key Location/Qualifiers		
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		CDT CDS (157) . (446) .		
		FEATURES Source 1. . 446 /organism="Dahlia merckii"		
		/mol type="genomic DNA"		
		/db_Xref="taxon:43367"		
		ORIGIN		

ORIGIN							
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Qy	1 ATGGTGAATCGGTGCGTCCGGTTCGGTCTGATCCRTTCTGCTCGCTGCCATC	0;	Indels 0;	Gaps 0;			
Db	1 ATGGTGAATCGGTGCGTCCGGTTCGGTCTGATCCRTTCTGCTCGCTGCCATC	60					
Qy	61 TCAGGTTATAAATCCTTAACTTCAATTGAAATATGATAGTTATTATCTTTATGG	120					
Db	61 TCAGGTTATAAATCCTTAACTTCAATTGAAATATGATAGTTATTATCTTTATGG	120					
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Db	121 TTTATGTTCTGACAAGTGCATAATTGAGTAGATATGCACTCGTTAGTGAGAAC	180					
Qy	181 TATGGAGAAGACTGACCAAGCATGTCGGAAACTGTGGCAATACGGGACATTGTGACA	240					
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Db	301 ACATGTGTTCTGTACTTCAATTGTAAGGCGAAAGCTTGCTCAAGACAACCTTA	360					
Qy	361 AAGCGAACACTCGCTCAAGACAACACTTAATGCCAAAAGCTTGACCGTGTGCCAAGA	420					
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Db	421 AAGTGGTTCCAACGTTGACATCCG 446						
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BD240919	BD240919	Polyimide sequence <sub>B</sub>	446 bp	DNA	linear	PAT 17-JUL-2003	
LOCUS	DEFINITION	Polyimide sequence <sub>B</sub>					
BD240919	ACCESSION						
BD240919.1	VERSION						
JP 200223052-A/5	KEYWORDS						
Dahlia merckii (bedding dahlia)	SOURCE						
Dahlia merckii	ORGANISM						
Eukaryota; Viridiplantae; Streptophytina; Embryophytina; Tracheophytina; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; campanulids; Asterales; Asteraceae; Asteroideae; Coreopsidae; Dahlia.	REFERENCE						
Evans, I.J. and Ray, J.A. (bases 1 to 446)	AUTHORS						
Patent: JP 200223052-A 5 30-JUL-2002;	TITLE						
SYNGETA LTD	JOURNAL						
Dahlia merckii (dahlia)	COMMENT						
JP 200223052-A/5	OS	Artificial Sequence					
PN	PN	JP 200223047-A/5					
PD 30-JUL-2002	DEFINITION						
PP 17-AUG-1999 JP 20000566448	ACCESSION						
PP 18-AUG-1999 JP 20000566429	VERSION						
IAN JEFFREY EVANS JOHN ANTHONY RAY C12N5/09, A01H5/00, C01K14/115, C12N5/10 // (C12N5/10, C12R1:91), C12N5/00, (C12N5/00, C12R1:91)	KEYWORDS						
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FH Key	Location/Qualifiers						
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FT CDS (157) . (446)	Location/Qualifiers						
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REFERENCE	1	Qy	215	CTGTGCCAATACGGGACATTGTGACAACCAATGTAAATCATGGGAGGTGGCCCATGG	274
AUTHORS	Miao, G.H., Weng, Z. and Famodu, O.O.	Db	140	CTGTGCCAATACGGGACACTGTGACAACCAATGTAAATCATGGGAGGTGGCCCATGG	199
TITLE	Plant defensins	Db	140	CTGTGCCAATACGGGACACTGTGACAACCAATGTAAATCATGGGAGGTGGCCCATGG	199
JOURNAL	Patent: WO 0068405-A 3 16-NOV-2000;	Qy	275	AGCGTGTCACTGTGGTAACCGGAACACACATGTGTTCTGTACTCTAACAAAGC	334
FEATURES	E.I. DU PONT DE NEMOURS AND COMPANY (US)	Db	200	TGCGTGTCACTGTGGTAACCGGAACACACATGTGTTCTGTACTCTAACAAAGC	259
source	Location/Qualifiers	Qy	335	CGAAAGCTTGCTCAAGACAACATAAGCGTCAAGACAACACTTAATG	393
1.. .460	/organism="Dimorphotheca sinuata"	Db	260	CGAAAGCTTGCTCAAGACAACATAAGCGTCAAGACAACACTTAATG	318
/mol_type="unassigned DNA"	/db_xref="taxon:112408"				
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Query Match	37.8%; Score 168.6; DB 6; Length 460;				
Best Local Similarity	81.6%; Pred. No. 6.3e-33;				
Matches	195; Conservative 0; Mismatches 44; Indels 0; Gaps 0;				
	RESULT 15				
	LOCUS BD22237	BD22237	534 bp	DNA linear	PAT 17-JUL-2003
	DEFINITION Method of genetic expression of polyprotein in plant.				
	ACCESSION BD22237				
	VERSION BD22237.1				
	KEYWORDS JP 2002523047-A/6				
	SOURCE synthetic construct				
	ORGANISM other sequences; artificial sequences.				
	REFERENCE 1 (bases 1 to 53)				
	AUTHORS Broekaert, W.P., Francois, I.E.J.A., Bolle, M.F.C.D., Evans, I.J. and Ray, J.A.				
	TITLE Method of genetic expression of polyprotein in plant				
	JOURNAL Patent: JP 2002523047-A 6 30-JUL-2002;				
	COMMENT OS Artificial Sequence				
	PN JPP 2002523047-A/6				
	PD 30-JUL-2002				
	PP 1 AUG-1999 JP 2000566429				
	PR 18 AUG-1998 GB 9818001.1, 04-DEC-1998 GB 9826753.7 PI				
	DEFINITION WILLEM FRANS BROEKAERT, ISABELLE ELSA JEANNE				
	SEQUENCE AUGUSTINE FRANCOIS,				
	VERSION PI MIGUEL FRANCESCO COLETA DE BOLLE, IAN JEFFREY EVANS, JOHN PI				
	KEYWORDS ANTHONY RAY				
	SOURCE PC C12N15/09, A01H1/00, C07K1/12, C12N5/10, C12P21/02// (C12N5/10, PC C12N15/09, A01H1/00, C07K1/12, C12N5/10, C12P21/02// (C12N5/10, PC C12N15/00, C12N5/00, C12R1:91)				
	FEATURES CC Description of Artificial Sequence: Synthetic sequence FH				
	ORIGIN Key CDS Location/Qualifiers				
	COMMENT FT (76) . (525).				
	FEATURES source Location/Qualifiers				
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	/mol_type="genomic DNA"				
	/db_xref="taxon:32630"				
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DEFINITION Sequence 1 from Patent WO0068405.					
ACCESSION AX046743					
VERSION AX046743.1					
KEYWORDS GI:11876280					
SOURCE Dimorphotheca sinuata (African daisy)					
ORGANISM Dimorphotheca sinuata					
SOURCE Viridiplantae; Streptophytina; Embryophytina; Tracheophytina; Spermatophytina; Magnoliophytina; eu dicotyledons; core eudicots; asterids; campanulids; Asterales; Asteraceae; Asteroideae; Calenduleae; Dimorphotheca.					
REFERENCE 1.. .503 /organism="Dimorphotheca sinuata"					
AUTHORS Miao, G.H., Weng, Z. and Famodu, O.O.					
TITLE Plant defensins					
JOURNAL Patent: WO 0068405-A 1 16-NOV-2000;					
FEATURES source Location/Qualifiers					
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unsure	349	Db 138 AGATTCGCAATACGGGACATTGTGACAACCAATGTAAATCATGGGAGGTAGCAAGACATGGTCGGCAA	197		
unsure	416	Qy 215 CTGTGCCAATACGGGACATTGTGACAACCAATGTAAATCATGGGAGGTGGCCCATGG	274		
unsure	458	Db 198 CTGTGCCAATACGGGACATTGTGACAACCAATGTAAATCATGGGAGGTGGCCCATGG	257		
unsure	474	Qy 275 AGCGTGTCACTGTGGTAACGGGAAACATGTGACAACACTTAATGTTCTGTACTCTAACATGT	326		
unsure	479	Db 258 AGCGTGTCACTGTGGTAACGGGAAACATGTGACAACACTTAATGTTCTGTACTCTAACATGT	309		
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Best Local Similarity 81.6%; Pred. No. 6.3e-33;					
Matches 195; Conservative 0; Mismatches 44; Indels 0; Gaps 0;					
Qy 155 AGATATCCCATCGGTAGTGGGAAACTATGGGAAAGCTACCAAGACATGGTCGGAAA	214				
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Search completed: March 18, 2005, 14:31:02  
Job time : 2320 secs

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XX 02-MAR-2000.  
 PD 17-AUG-1999; 99WO-GB002720.  
 XX PR 18-AUG-1998; 98GB-00018003.  
 XX PA (ZENECA LTD.  
 XX PT Evans IJ, Ray JA;  
 XX PS WPI; 2000-237658/20.  
 DR P-PSDB; AA470315.  
 XX PT Polynucleotide sequences and expression products useful for producing  
 XX transgenic plants that are resistant to microbial infections.  
 PS Claim 1; Fig 1A; 77pp; English.  
 XX CC The present sequence is a Dahlia merckii cDNA encoding an antimicrobial  
 CC preprotein Dm-AMP1. This sequence is useful in the production of  
 CC transgenic plants which show improved resistance to infections by  
 CC microorganisms such as bacteria and fungi. Transgenic plants include e.g.  
 CC field crops, fruits and vegetables, such as canola, sunflower, tomato,  
 CC apple, banana, pear and mango.  
 XX SQ Sequence 446 BP; 128 A; 86 C; 104 G; 128 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 446; DB 3; Length 446;  
 Best Local Similarity 100.0%; Pred. No. 9.9e-113;  
 Matches 446; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 ATGGTGAATCGGTGCGCTCTCGGTGCGTCGTTCTGATCCRTTGATC 60  
 Db 1 ATGGTGAATCGGTGCGCTCTCGGTGCGTCGTTCTGATCCRTTGATC 60  
 Qy 61 TCAGGGTTACAATCTTAGTCAATTGAAATATGATACTTATCTTATGG 120  
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 Qy 121 TTATATGTTCTGACAGTGTGCAAATATTAGTCAATTGCACTGGTAGTGGAAAC 180  
 Db 121 TTATATGTTCTGACAGTGTGCAAATATTAGTCAATTGCACTGGTAGTGGAAAC 180  
 Qy 181 TATGCCGAAAAGCTAGAACATGGTCAAGCATGGTCAACTGGGAACTGGGAAAC 240  
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 Qy 241 ACCAATGAAATCAATCATGGGAGGTGGGAGGTGGCCATGGACATGGTCAAGAAC 300  
 Db 241 ACCAATGAAATCAATCATGGGAGGTGGGAGGTGGCCATGGACATGGTCAAGAAC 300  
 Qy 301 ACATGTGTTCTGTTACTTCATTGTAAGGCGAAAGCTTCTGAGACAACTTA 360  
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 Qy 361 AAGCCGAAACAACCTGCTAACAGAACATTATGCCAAAGCTTGCATGGCAAGA 420  
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 Best Local Similarity 100.0%; Pred. No. 9.9e-113;  
 Matches 446; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 Db 1 ATGGTGAATGGTCTGGTTCTGGCTTCTGATCCCTTCTGCTCCCATC 60  
 Qy 61 TCAGGGTTACAATCTTACTTCATTATGAAATGATGAGTATTATCTTATGG 120  
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 Qy 121 TTTTATGTTCTGATGCAAGCTTACCTGATGCAAGAAATTTGAGTGGAAAC 180

DE DNA encoding the Dahlia antimicrobial protein 1 (AMP1).  
 XX KW Antimicrobial protein; AMP1; transgenic plant; linker propeptide;  
 KW protein expression; ss.  
 XX OS Dahlia merckii.  
 XX XX Key FH  
 CDS FT  
 FT /\*tag= a  
 FT /note= 'contains 1 intron; no termination codon'  
 FT exon 1.  
 FT /\*tag= b  
 FT /number= 1  
 FT intron 65..156  
 FT /\*tag= c  
 FT /number= 1  
 FT exon 157..446  
 FT /\*tag= d  
 FT /number= 2  
 FT mat\_peptide 177..314  
 FT /\*tag= e  
 PN WO200011175-A1.  
 XX XX PD 02-MAR-2000.  
 XX XX PP 17-AUG-1999;  
 XX XX PR 18-AUG-1998;  
 PR 04-DEC-1998;  
 XX PA (ZENECA LTD.  
 XX XX PI Broekaert WF, Francois IEJA, De Bolle MFC, Evans IJ, Ray JA;  
 DR WPI; 2000-246564/21.  
 DR P-PSDB; AAY84050.  
 XX PT Improving expression of polyproteins in plants involves coexpression of  
 two or more proteins in plants within a single transcription unit.  
 XX PS Example 1; Fig 1; 151pp. English.  
 CC The present sequence encodes a Dahlia antimicrobial protein (AMP) 1. The  
 CC AMP protein is used to produce transgenic plants, using the method of  
 CC the invention. The specification describes methods for improving  
 CC expression levels of one or more proteins in a transgenic plant. The  
 CC method comprises inserting a DNA sequence having a promoter region  
 CC operably linked to two or more protein encoding regions separated by a  
 CC DNA sequence coding for a linker propeptide and a terminator region. The  
 CC method is used to produce proteins in plants. The linker propeptide  
 CC comprising a cleavage site, whereby the expressed polypeptide is post-  
 CC translationally processed into the component protein molecules. The  
 CC propeptide sequence is rich in amino acids A, V, S and T and contains  
 CC dipeptidic sequences consisting of either two acidic, two basic or one  
 CC acidic and one basic residue as a cleavable linker sequence  
 XX SQ Sequence 446 BP; 128 A; 86 C; 104 G; 128 T; 0 U; 0 Other;  
 RESULT 2  
 AAZ9323  
 ID AAZ9323 standard; DNA; 446 BP.  
 XX AC AAZ9323;  
 DT 03-JUL-2000 (First entry)



XX Broekaert WF, Francois IEJA, De Bolle MFC, Evans IJ, Ray JA; /product= "Antimicrobial protein"

XX WPI: 2000-246564/21. PN WO200111196-A1.

DR P-PSDB; AAY84069. XX PD 02-MAR-2000.

XX Improving expression of polyproteins in plants involves coexpression of PT two or more proteins in plants within a single transcription unit. XX PP 17-AUG-1999; 99WO-GB002720.

PT Disclosure; Fig 31; 151pp; English. XX PR 18-AUG-1998; 98GB-00018003.

CC The present sequence encodes a protein of the invention, comprising the mature proteins of the plant defensins, the Dahlia antimicrobial protein (AMP) 1 and the antifungal protein 2 (RsAFP2), linked by a linker propeptide of the invention. The specification describes methods for improving expression levels of one or more proteins in a transgenic plant. The method comprises inserting a DNA sequence having a promoter by a DNA sequence coding for a linker propeptide and a terminator region. The method is used to produce proteins in plants. The linker propeptide comprising a cleavage site, whereby the expressed polyprotein is post-translationally processed into the component protein molecules. The propeptide sequence is rich in amino acids A, V, S and T and contains dipeptidic sequences consisting of either two acidic, two basic or one acidic and one basic residue as a cleavable linker sequence.

XX SQ Sequence 557 BP; 164 A; 122 C; 143 G; 128 T; 0 U; 0 Other;

Query Match 63.7%; Score 284; DB 3; Length 557; Best Local Similarity 98.3%; Pred. No. 4.5e-68; Matches 287; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 155 AGATATCGCATCGTTAGTGAGAAACTATGGCAGAAAGCTAGTGTCCGGAAA 214 Db 65 AGATATCGCATCGTTAGTGAGAAACTATGGCAGAAAGCTAGTGTCCGGCAA 124

Qy 215 CTGGGCAATACTGGGACTTGTGACAAACAAATCATGGAGGGTGGGCCATGG 274 Db 125 CTGGGCAACAGGGACTTGTGACAAACAAATCATGGAGGGTGGCCATGG 184

Qy 275 AGCGTGTCAATCGCTCAAGAACATGTTCTGTTACTTCATGTTAAAGGC 334 Db 185 AGCGTGTCAATCGCTCAAGAACATGTTCTGTTACTTCATGTTAAAGGC 244

Qy 335 CGAAAAGCTTGTCAAGAACATTAAGGCCAACACTCGCTCAAGAACCTTAATGC 394 Db 245 CGAAAAGCTTGTCAAGAACATTAAGGCCAACACTCGCTCAAGAACCTTAATGC 304

Qy 395 CGAAAAGCTTGTCAAGAACATTAAGGCCAACACTCGCTCAAGAACATCCG 446 Db 305 CGAAAAGCTTGTCAAGAACATTAAGGCCAACACTCGCTCAAGAACATCCG 356

XX AC AA251396 standard; DNA: 534 BP.

XX AC AA251396; DT 06-JUN-2000 (first entry)

DB Portion of pFAJ3106 encoding Dahlia merckii antimicrobial protein.

KW Antimicrobial protein; DmAMP; transgenic plant; microbial infection/bacteria; fungi; field crop; fruit; vegetable; canola; banana; sunflower; apple; plant transformation vector; db.

XX OS Dahlia merckii.

XX Key Location/Qualifiers

FH 76. .525

FT /\*tag= a

XX OS Synthetic.

XX OS Unidentified.

XX AC AA25139325 standard; DNA: 534 BP.

XX AC AA25139325; DT 03-JUL-2000 (first entry)

DB DNA encoding a fusion protein of DmAMP1 and RbAFP2.

KW Antimicrobial protein; AMP; transgenic plant; linker propeptide; protein expression; plant defensin; RbAFP2; antifungal protein; AFP2; ss.

XX KW Synthetic.

OS Dahlia merckii.

XX OS Unidentified.

XX FH Key

FT CDS 76. .522

FT /\*tag= a

PT misc\_feature 160 .309  
 PT /\*tag= b  
 /note= "encodes DmAMP1"  
 PT misc\_feature 370 .538  
 PT /\*tag= C  
 /note= "encodes RsAFP2"  
 PT XX WO200011175-A1.  
 XX PD 02-MAR-2000.  
 XX PP 17-AUG-1999; 99WO-GB0022716.  
 XX PR 18-AUG-1998; 98GB-00018001.  
 PR 04-DEC-1998; 98GB-00026753.  
 XX PA (ZENE ) ZENECA LTD.  
 XX WPI; 2000-246564/21.  
 DR P-PSDB; AAY84058.  
 XX PT Improving expression of polyproteins in plants involves coexpression of two or more proteins in plants within a single transcription unit.  
 XX PS Example 2; Fig 9; 151pp; English.  
 XX CC The present sequence encodes a protein of the invention, comprising the mature proteins of the plant defensins, the Dahlia antimicrobial protein (AMP) 1 and the antifungal protein 2 (AFP2), linked by a linker propeptide of the invention. The specification describes methods for improving expression levels of one or more proteins in a transgenic plant. The method comprises inserting a DNA sequence having a promoter region operably linked to two or more protein encoding regions separated by a DNA sequence coding for a linker propeptide and a terminator region. The method is used to produce proteins in plants. The linker propeptide comprising a cleavage site, whereby the expressed polypeptide is post-translationally processed into the component protein molecules. The propeptide sequence is rich in amino acids A, V, S and T and contains dipeptidic sequences consisting of either two acidic, two basic or one acidic and one basic residue as a cleavable linker sequence  
 XX Sequence 534 BP; 164 A; 118 C; 122 G; 130 T; 0 U; 0 Other;  
 SQ Query Match Score 215.2; DB 3; Length 534;  
 Best Local Similarity 98.6%; Pred. No. 4e-49;  
 Matches 217; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Qy 155 AGATATCCATCGTTACTGGAAACTATGGAAAGCTAGCAAGAACATGGTGGGAAA 214  
 Db 138 AGATATCCATCGTTACTGGAAACTATGGAAAGCTAGCAAGGTGGTGGGAAA 197  
 Qy 215 CNGTGGCATATACTGGACAACTGACATGGGACATTGACAACTGTAATCATGGGGGTGGGCCCATGG 274  
 Db 198 CNTGGCATACGGGACATTGACACAACTGTAATCATGGGGGTGGGCCCATGG 257  
 Qy 275 AGGGTGATATGTCGTTACGGAAACATGGGACATTGACATGGGGGTGGGCCCATGG 334  
 Db 258 AGGGTGATATGTCGTTACGGAAACATGGGACATTGACACAACTGTAATCATGGGGGTGGGCCCATGG 317  
 Qy 335 CGAAAAGCTGGTCAAGACAAACTTAAGGCCAACACTC 374  
 Db 318 CGAAAAGCTGGTCAAGACAAACTTAAGGCCAACACTC 357  
 Qy 403 CGAAAAGCTGGTCAAGACAAACTTAAGGCCAACACTC 374  
 Db 395 CGAAAAGCTGGTCAAGACAAACTTAAGGCCAACACTC 284  
 DT 03-JUL-2000 (first entry)

XX DNA encoding a fusion protein of DmAMP1 and RsAFP2.  
 DE XX  
 XX KW Antimicrobial protein; AMP1; transgenic plant; linker propeptide;  
 KW protein expression; plant defensin; RsAFP2; antifungal protein; AFP2; 68.  
 XX Synthetic.  
 OS Dahlie merckii.  
 OS Unidentified.

XX Key Location/Qualifiers  
 FH 3. .476  
 CDS /\*tag= a  
 /product= "fusion protein of DmAMP1 and RsAFP2"  
 XX PN WO200011175-A1.  
 XX PD 02-MAR-2000.  
 XX PF 17-AUG-1999; 99WO-GB0022716.  
 XX PR 18-AUG-1998; 98GB-00018001.  
 PR 04-DEC-1998; 98GB-00026753.  
 XX PA (ZENE ) ZENECA LTD.  
 XX PI Broekaert WF, Francois IEJA, De Bolle MFC, Evans IJ, Ray JA;  
 XX WPI; 2000-246564/21.  
 DR P-PSDB; AAY84058.  
 XX PT Improving expression of polyproteins in plants involves coexpression of two or more proteins in plants within a single transcription unit.  
 XX PS Disclosure; Fig 30; 151pp; English.  
 XX CC The present sequence encodes a protein of the invention, comprising the mature proteins of the plant defensins, the Dahlia antimicrobial protein (AMP) 1 and the antifungal protein 2 (RsAFP2), linked by a linker propeptide of the invention. The specification describes methods for improving expression levels of one or more proteins in a transgenic plant. The method comprises inserting a DNA sequence having a promoter region operably linked to two or more protein encoding regions separated by a DNA sequence coding for a linker propeptide and a terminator region. The method is used to produce proteins in plants. The linker propeptide comprising a cleavage site, whereby the expressed polypeptide is post-translationally processed into the component protein molecules. The propeptide sequence is rich in amino acids A, V, S and T and contains dipeptidic sequences consisting of either two acidic, two basic or one acidic and one basic residue as a cleavable linker sequence  
 XX SQ Sequence 485 BP; 139 A; 104 C; 128 G; 114 T; 0 U; 0 Other;  
 Query Match Score 47.5%; DB 3; Length 485;  
 Best Local Similarity 97.7%; Pred. No. 3e-48;  
 Matches 215; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 Qy 155 AGATATCCATCGTTACTGGAAACTATGGAAAGCTAGCAAGAACATGGTGGGAAA 214  
 Db 65 AGATATCCATCGTTACTGGAAACTATGGAAAGCTAGCAAGAACATGGTGGGAAA 124  
 Qy 215 CTGTGGCATATGGACATTGACACAACTGTAATCATGGGGGTGGGCCCATGG 274  
 Db 125 CTGTGGCATACGGGACATTGACACAACTGTAATCATGGGGGTGGGCCCATGG 184  
 Qy 275 AGGGTGATATGTCGTTACGGAAACATGGGACATTGACATGGGGGTGGGCCCATGG 334  
 Db 185 AGGGTGATATGTCGTTACGGAAACATGGGACATTGACACAACTGTAATCATGGGGGTGGGCCCATGG 244  
 Qy 335 CGAAAAGCTGGTCAAGACAAACTTAAGGCCAACACTC 374  
 Db 395 CGAAAAGCTGGTCAAGACAAACTTAAGGCCAACACTC 284  
 DT 03-JUL-2000 (first entry)

RESULT 7  
 AAZ99335 standard; DNA; 485 BP.  
 ID AAZ99335  
 AC XX  
 XX  
 DT 03-JUL-2000 (first entry)

RESULT 8	Qy	395 CCAAAGCTTGACCGTGTATGCCAAGAAAGTGGTCCAAAGTGTGACATCC 445
ADM77231	Db	318 AGATACTTGTACCATGATGCCAAGAAAGTGTGACATCC 368
TD ADM77231 standard; cDNA; 529 BP.		
XX		
AC ADM77231;		
XX		
DT 03-JUN-2004 (first entry)		RESULT 9
XX		ADM77214
DE Ironweed cDNA encoding mature defensin #2.		ID ADM77214 standard; cDNA; 579 BP.
XX		XX
KW Ironweed; ss; EST; expressed sequence tag; defensin;		AC ADM77214;
KW soybean cyst nematode; pesticide; plant; plant pathogen;		XX
KW sclerotinia sclerotiorum; fungal infection; Candidiasis.		DT 03-JUN-2004 (first entry)
XX		DB Ironweed cDNA encoding mature defensin #1.
OS Vernonia mespiliifolia.		KW Ironweed; ss; EST; expressed sequence tag; defensin;
XX		KW soybean cyst nematode; pesticide; plant; plant pathogen;
PN US2003140368-A1.		KW sclerotinia sclerotiorum; fungal infection; Candidiasis.
XX		XX
PD 24-JUL-2003.		OS Vernonia mespiliifolia.
XX		XX
PP 21-JUN-2002; 2002US-00178449.		PN US2003140368-A1.
XX		XX
PR 25-OCT-2001; 2001US-00030516.		PD 24-JUL-2003.
XX		XX
PA (PIONEER) PIONEER HI-BRED INT INC.		21-JUN-2002; 2002US-00178449.
XX		PP
PI Fahodou OO, Herrmann R, Lu AL, Mccutchen BF, Miao G, Presnail JK;		PR 25-OCT-2001; 2001US-00030516.
PI Rafalski JA, Weng Z;		XX
DR WPI; 2003-851760/79.		PA (PIONEER) PIONEER HI-BRED INT INC.
XX		XX
P-PSDB; ADM77232.		PI Fahodou OO, Herrmann R, Lu AL, Mccutchen BF, Miao G, Presnail JK;
XX		PI Rafalski JA, Weng Z;
PT New nucleic acid molecule, useful for preparing a composition for		XX
PT treating fungal infections, e.g. Candidiasis.		WPI; 2003-851760/79.
XX		DR P-PSDB; ADM77232.
PS Claim 1; SEQ ID NO 48; 69pp; English.		XX
XX		PT New nucleic acid molecule, useful for preparing a composition for
CC treating fungal infections, e.g. Candidiasis.		XX
CC The invention relates to an isolated nucleic acid molecule (either an		PT treating fungal infections, e.g. Candidiasis. The present sequence is either an
CC EST, expressed sequence tag or an EST contig) encoding a plant defensin		XX
CC or its mature form, or the complement of them. Also included are a DNA		PS Claim 1; SEQ ID NO 31; 69pp; English.
CC construct comprising the novel nucleic acid (operably linked to a		XX
CC promoter that drives expression in a host cell), an expression cassette		CC The invention relates to an isolated nucleic acid molecule (either an
CC comprising the DNA construct, a host cell having stably incorporated into		CC EST, expressed sequence tag or an EST contig) encoding a plant defensin
CC its genome the DNA construct, an isolated polypeptide and impacting a		CC or its mature form, or the complement of them. Also included are a DNA
CC plant pathogen e.g. soybean cyst nematode (Sclerotinia sclerotiorum). The		CC construct comprising the novel nucleic acid (operably linked to a
CC nucleic acid construct is useful for preparing a composition for treating		CC promoter that drives expression in a host cell), an expression cassette
CC fungal infections, e.g. Candidiasis. The present sequence is either an		CC comprising the DNA construct, a host cell having stably incorporated into
CC EST (expressed sequence tag) or an EST contig encoding a plant defensin		CC its genome the DNA construct, an isolated polypeptide and impacting a
CC or its mature form.		CC plant pathogen e.g. soybean cyst nematode (Sclerotinia sclerotiorum). The
CC nucleic acid construct is useful for preparing a composition for treating		CC nucleic acid construct is useful for preparing a composition for treating
CC fungal infections, e.g. Candidiasis. The present sequence is either an		CC fungal infections, e.g. Candidiasis. The present sequence is either an
CC EST (expressed sequence tag) or an EST contig encoding a plant defensin		CC EST (expressed sequence tag) or an EST contig encoding a plant defensin
CC or its mature form.		CC or its mature form.
SQ Sequence 529 BP; 178 A; 88 C; 111 G; 148 T; 0 U; 4 Other;		XX
Best Local Similarity 47.0%; Score 209.4; DB 11; Length 529;		Query Match 45.5%; Score 403; Best Local Similarity 81.1%; Pred. No. 9
Matches 240; Conservative 0; Mismatches 51; Indels 0; Gaps 0;		5.5%; Length 579;
Qy 155 AGATATCGCATCGTTAGTGGAGAACTATGGGAGAAGCTGGTCGGAAA 214		Best Local Similarity 81.1%; Pred. No. 9 5e-46; Matches 236; Conservative
Db 78 AGAAATCTCGACTGTGAGAGAGCTATGGCAAGCTGGCA 137		0; Mismatches 55; Indels 0; Gaps 0;
Qy 215 CTGTGGCAATACGGGACATTGTGACACATGTGAATCATGGAAAGGGGGCCATGG 274		Qy 155 AGATATCGCATCGTTAGTGGAGAACTATGGGAGAAGCTGGTCGGAAA 214
Db 138 CTGTGGCAACAGGACATTGTGATCATGTGAACTGGGGGGCAGGCCATGG 197		Db 92 AGAAATCTCGACTGTGAGAGAGCTATGGCAAGAGCTGGTCAGGCAA 151
Qy 275 AGCGTGTCACTGTGCGTAACGGAAAACAATGTGTTCTGTACTCTCAATTGTAAAGAC 334		Qy 215 CTGTGGCAATACGGGACATTGTGACACATGTGAATCATGGAGGTGGCCCATGG 274
Db 198 ACCTTCATGTGCGGGGAACACATGTGTTCTGTACTCTCAATTGTAAAGAC 257		Db 152 CTGTGGCAACAGGACATTGTGATCATGTGAACTGGGGGGCAGGCCATGG 211
Qy 335 CGAAAAGCTGTGCTCAAGAACACATTAAGGCCAAACATTAAGCTAACTTAATG 394		Qy 275 AGCGTGTCACTGTGCGTAACGGAAAACAATGTGTTCTGTACTCTCAATTGTAAAGAC 334
Db 258 TGAAAAACTCGCTCAAGATAAGCTAAAGCAGAAGCTGTCAAGAACACTCAAGGC 317		Db 212 ACCTTCATGTGCGGGGAACACATGTGTTCTGTACTCTCAATTGTAAAGAC 271

Qy	335 CGAAAAGCTTGCCTCAAGACAACACTAAAGCCGAAACACTCGCTCAAGACAACACTATGTC 394	Qy	155 AGATATGCCATCGCTTAGTGGAAACTATGGGAGAACATGTGGAAAGCTAGCAAGACATGTGGAAA 214
Db	272 TGAATAAACCTCGCTTCAGATGTTAAGCTTAAGCTTAAGCTTAAGCTTAAGCTAACACTCAAGGC 331	Db	82 AGATATCACAGTGAGGAAAGTATGGAGAACATGTGGAAAGCTAACACTCAAGGC 141
Qy	395 CCAAAGCTTGCCTGACCGTGTGGTTCCAACACCTTGAACATCC 445	Qy	215 CTGTCGCAATACGGGACATCTGCAACACCATGTAATCATGGAAAGGTGGGCCCATGG 274
Db	332 AGATAACTTGTACCATGATGCAAAAGTAGTACCAATGTCGAACATCC 382	Db	142 CTGTCGCAACAGGGACACTGTGACCAACCATTGAAATCTGGAAAGGTGGGCCCATGG 201
<b>RESULT 10</b>			
AAZ51378		Qy	275 AGCGTTTCATGTGGTAACCGGAAACACATGTGTTCTGTACTCTATGTAAGAAAGC 334
ID AAZ51378	standard; cDNA; 577 BP.	Db	202 GGCGTGCACCTGCGTGGAGGAAACACATGTGTTCTGTACTCTAAGTGTCCAAAGC 261
XX		Qy	335 CGAAANGCTTGTCAAGACAAACTTAAGCGGAAAGACTCCTCAAGACAAACTATGTC 394
AC AAZ51378;		Db	262 CGAAANGCTT-----GCTCAAGACAAAGTAAATGTC 291
XX		Qy	395 CCAAAGCTTGCCTGAGGAAAGTGTGACATCCAAACGTTGACATCCG 446
DJ 06-JUN-2000	(first entry)	Db	292 CCAAGGCTTGTCAAGCGTATGCAAGAAAGTGTGACATCCG 343
XX	Dahlia merckii antimicrobial protein Dm2.5 cDNA.		
DE			
XX	Antimicrobial protein; DmAMP; Dm2.5; transgenic plant; microbial infection; bacteria; fungi; field crop; fruit; vegetable; canola; banana; sunflower; apple; ss.		
KW			
KW			
OS Dahlia merckii.			
XX			
FH	Location/Qualifiers		
PT	20. .346		
PT	*tag= a		
PT	/product= "Antimicrobial protein Dm2.5"		
PT	/note= "Preproprotein"		
PT	sig_peptide		
PT	20. .103		
PT	mat_peptide		
PT	104. .253		
PT	*tag= b		
PT	/product= "Mature Dm2.5 protein"		
PT	/note= "Encodes protein which may be used as cleavable linker in the co-expression of multiple proteins"		
PT	254. .343		
PT	*tag= c		
PT	/product= "Mature Dm2.5 protein"		
PT	/note= "Encodes protein which may be used as cleavable linker in the co-expression of multiple proteins"		
PT	254. .343		
PT	*tag= d		
XX	PN WO200011196-A1.		
XX	PD 02-MAR-2000.		
PF	17-AUG-1999; 99WO-GB002720.		
XX	PR 18-AUG-1998; 98GB-00018003.		
XX	PA (ZENE ) ZENECA LTD.		
XX	PI Evans IJ, Ray JA;		
XX	DR WPI: 2000-237658/20.		
XX	DR P-PSDB; AAY70314.		
PS	PT Polynucleotide sequences and expression products useful for producing transgenic plants that are resistant to microbial infections.		
PS	PT Claim 1: Fig 3; 77pp; English.		
XX	CC The present sequence is a Dahlia merckii cDNA encoding an antimicrobial preproprotein Dm2.5. This sequence is useful in the production of transgenic plants which show improved resistance to infections by microorganisms such as bacteria and fungi. Transgenic plants include e.g. field crops, fruits and vegetables, such as canola, sunflower, tomato, apple, banana, pear and mango		
SQ Sequence 577 BP; 178 A; 96 C; 140 G; 163 T; 0 U; 0 Other; Score 177.2; DB 3; Length 577; Pred. No. 1.2e-38; Indels 30; Gaps 1;			
CC Best Local Similarity 80.1%; Conservative 0; Mismatches 28; Matches 234; Conservative 0; Mismatches 0; Gaps 0;			
CC Matches 234; Conservative 0; Mismatches 0; Gaps 0;			
CC Query Match 39.7%; Score 177.2; DB 3; Length 577; Pred. No. 1.2e-38; Indels 30; Gaps 1;			
CC The method comprises inserting a DNA sequence having a promoter region operably linked to two or more protein encoding regions separated by a DNA sequence coding for a linker peptide and a terminator region. The method is used to produce proteins in plants. The linker peptide			
XX Disclosure; Fig 28; 151pp; English.			
XX PT Improving expression of polyproteins in plants involves coexpression of two or more proteins in plants within a single transcription unit.			
XX CC The present sequence encodes a protein of the invention, comprising the mature proteins of the plant defensins, the Dahlia antimicrobial protein CC (AMP) 1 and the antifungal protein 2 (AFP2), linked by a linker CC peptide of the invention. The specific embodiment described methods for CC improving expression levels of one or more proteins in a transgenic CC plant. The method comprises inserting a DNA sequence having a promoter CC region operably linked to two or more protein encoding regions separated CC by a DNA sequence coding for a linker peptide and a terminator region. CC The method is used to produce proteins in plants. The linker peptide			
XX DR WPI; 2000-246564/21.			
XX DR P-PSDB; AAY84063.			

CC comprising a cleavage site, whereby the expressed polyprotein is post-  
 CC translationally processed into the component protein molecules. The  
 CC propeptide sequence is rich in amino acids A, V, S and T and contains  
 CC dipeptidic sequences consisting of either two acidic, two basic or one  
 XX acidic and one basic residue as a cleavable linker sequence

Sequence 485 BP; 124 A; 107 C; 128 G; 126 T; 0 U; 0 Other;

Query Match 38.8%; Score 173.2; DB: 3; Length 485;  
 Best Local Similarity 85.1%; Pred. No. 1.5e-37;  
 Matches 206; Conservative 0; Mismatches 33; Indels 3; Gaps 1;

Qy 155 AGATATGCATCCGTTAGTGCGAAACTATCGAGAAAGCTAGAACATGGTGGAAA 214  
 Db 65 AGATATGCATCGTTAGTGCGAAACTATCGAGAAAGCTAGAACATGGTGGAAA 124  
 Qy 215 CTGTGCGAACTACGGGACATTGTCGAAACCATTGTAATCATGGGAGGTGCGCCATGG 274  
 Db 125 CTGTGCGAACTACGGGACATTGTCGAAACCATTGTAATCATGGGAGGTGCGCCATGG 184  
 Qy 275 AGCGGTTCACTGTGCCATACTGGAAACACATGGTTCTGTTACTTCATTGTAAGGC 334  
 Db 185 AGCGGTTCACTGTGCCATACTGGAAACACATGGTTCTGTTACTTCATTGTCAGC 244  
 Qy 335 CGAAAGCTGTCTGCTCAAGACAACATTAAG---CGGAAACACTGCTCAAGAAACTTAA 391  
 Db 245 TGAGGAAGCTGCTGCTGCTGTTCTGAACTCTGAACTTGTCAGAACTGAGAAGTCC 304  
 Qy 392 TG 393  
 Db 305 TG 306

RESULT 12  
 AA229329 AA229329 standard; DNA; 446 BP.  
 XX  
 AC AA229329;  
 DT 03-JUL-2000 (first entry)  
 XX  
 DE DNA encoding a fusion protein of DmAMP1 and RsaAFP2.  
 XX  
 KW Antimicrobial protein; AMP1; transgenic plant; linker propeptide;  
 protein expression; plant defensin; RsaFP2; antifungal protein; AFP2; 88.  
 XX  
 OS Synthetic.  
 OS Dahlia merckii.  
 OS Unidentified.

Key FH Location/Qualifiers  
 CDS 3..437 /tag= a  
 PR /product= "fusion protein of DmAMP1 and RsaFP2"  
 PN WO200011175-A1.  
 XX  
 PD 02-MAR-2000.  
 XX  
 PP 17-AUG-1999; 99WO-GB002716.  
 XX  
 PR 18-AUG-1998; 98GB-00018001.  
 PR 04-DEC-1998; 98GB-00026753.  
 XX  
 PA (ZENE ) ZENECA LTD.

XX  
 PP Brookaert WF, Francois IEJA, De Bolle MFC, Evans IJ, Ray JA;  
 XX  
 DR WPI: 2000-246564/21.  
 P-PSDB; ANY84062.  
 XX  
 PT Improving expression of polyproteins in plants involves coexpression of  
 two or more proteins in plants within a single transcription unit.

XX Disclosure; Fig 24; 151pp; English.  
 PS The present sequence encodes a protein of the invention, comprising the Dahlia antimicrobial protein  
 XX CC mature proteins of the plant defensins, the Dahlia antimicrobial protein  
 CC (AMP) 1 and the antifungal protein 2 (AFP2), linked by a linker  
 CC propeptide of the invention. The specification describes methods for  
 CC improving expression levels of one or more proteins in a transgenic  
 CC plant. The method comprises inserting a DNA sequence having a promoter  
 CC region operably linked to two or more protein encoding regions separated  
 CC by a DNA sequence coding for a linker propeptide and a terminator region.  
 CC The method is used to produce proteins in plants. The linker propeptide  
 CC comprising a cleavage site, whereby the expressed polyprotein is post-  
 CC translationally processed into the component protein molecules. The  
 CC propeptide sequence is rich in amino acids A, V, S and T and contains  
 CC dipeptidic sequences consisting of either two acidic, two basic or one  
 CC acidic and one basic residue as a cleavable linker sequence  
 XX Sequence 446 BP; 111 A; 102 C; 123 G; 110 T; 0 U; 0 Other;

Query Match 38.6%; Score 172.2; DB: 3; Length 446;  
 Best Local Similarity 93.3%; Pred. No. 2.7e-37;  
 Matches 180; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 155 AGATATGCATCCGTTAGTGCGAAACTATGGGAAACCTGCGACAATGCGAGAATCTGGGAAA 214  
 Db 65 AGATATGCATCCGTTAGTGCGAAACTATGGGAAACCTGCGACAATGCGAGAATCTGGGAAA 124  
 Qy 215 CTGTGCGAACTACGGGACATTGTCGAAACCATTGTAATCATGGGAGGTGCGCCATGG 274  
 Db 125 CTGTGCGAACTACGGGACATTGTCGAAACCATTGTAATCATGGGAGGTGCGCCATGG 184  
 Qy 275 AGCGGTTCACTGTGCCATACTGGAAACACATGGTTCTGTTACTTCATTGTAAGGC 334  
 Db 185 AGCGGTTCACTGTGCCATACTGGAAACACATGGTTCTGTTACTTCATTGTCAGC 244  
 Qy 335 CGAAAGCTGTCTGCTCAAGACAACATTAAG---CGGAAACACTGCTCAAGAAACTTAA 391  
 Db 245 TGAGGAAGCTGCTGCTGCTGTTCTGAACTCTGAACTTGTCAGAACTGAGAAGTCC 304  
 Qy 392 TG 393  
 Db 305 TG 306

RESULT 13  
 AA229334 AA229334 standard; DNA; 1093 BP.  
 ID AA229334  
 AC AA229334;  
 XX  
 DT 03-JUL-2000 (first entry)  
 XX  
 DE DNA encoding a fusion protein of DmAMP1, RsaFP2, and AceAMP1.  
 XX  
 KW Antimicrobial protein; AMP1; transgenic plant; linker propeptide;  
 protein expression; plant defensin; RsaFP2; antifungal protein; AFP2; 88.  
 XX  
 OS Synthetic.  
 OS Dahlia merckii.  
 OS Unidentified.

Key FH Location/Qualifiers  
 CDS 3..437 /tag= a  
 PR /product= "fusion protein of plant defensins"  
 XX  
 PN WO200011175-A1.  
 XX  
 PD 02-MAR-2000.  
 XX  
 PP 17-AUG-1999; 99WO-GB002716.  
 XX  
 PR 18-AUG-1998; 98GB-00018001.  
 PR 04-DEC-1998; 98GB-00026753.  
 XX  
 PA (ZENE ) ZENECA LTD.

XX  
 Key Location/Qualifiers  
 CDS 3..1085  
 FT /\*tag= a  
 FT /product= "fusion protein of plant defensins"  
 XX  
 PN WO200011175-A1.  
 XX  
 PD 02-MAR-2000.  
 XX  
 PP 17-AUG-1999; 99WO-GB002716.  
 XX  
 PR 18-AUG-1998; 98GB-00018001.  
 PR 04-DEC-1998; 98GB-00026753.  
 XX  
 PA (ZENE ) ZENECA LTD.



XX Defensin; disease; fungus; resistance; transgenic plant; vaccine;  
 KW immunisation; antibody; crop protection; ds.  
 XX  
 OS Dimorphotheca sinuata.  
 XX  
 Key Location/Qualifiers  
 FH 25. .351  
 PT /\*tag= a  
 FT /product= "Plant defensin"  
 XX  
 PN WO200068405-A2.  
 XX  
 PD 16-NOV-2000.  
 XX  
 PP 03-MAY-2000; 2000WO-US011952.  
 XX  
 PR 07-MAY-1999;  
 XX 99US-01333039P.  
 PA (DUPO ) DU PONT DE NEMOURS & CO E I.  
 XX  
 PI Miao G, Weng Z, Famodu OO;  
 XX  
 DR 2001-024871/03.  
 DR P-PSDB; AAB04046.  
 XX  
 PT Isolated polynucleotides encoding plant defensins, useful for creating  
 PT transgenic plants with higher or lower levels of defensin polypeptides,  
 PT especially for increasing disease (e.g. fungal) resistance and stress  
 PT tolerance.  
 XX  
 PS Claim 2; Page 37; 50pp; English.  
 XX  
 CC Nucleotides encoding plant defensins can be used to create transgenic  
 CC plants in which plant defensin polypeptides are present at higher or  
 CC lower levels than normal, or in cell types or developmental stages in  
 CC which they are not normally found. This has the effect of altering the  
 CC level of disease (e.g. fungal) resistance and stress tolerance in those  
 CC cells. The defensin polypeptides are useful for immunising animals to  
 CC produce polyclonal or monoclonal antibodies. These antibodies are useful  
 CC for screening cDNA expression libraries to isolate full-length plant  
 CC defensin cDNA clones  
 XX  
 SQ Sequence 460 BP; 160 A; 83 C; 102 G; 115 T; 0 U; 0 Other;  
 CC  
 Query Match Score 168 6; DB 5; Length 460;  
 Best Local Similarity 81.6%; Pred. No. 2.6e-36;  
 Matches 195; Conservative 0; Mismatches 44; Indels 0; Gaps 0;  
 Qy 155 AGATAATCGCATCCGTTAGTGGAGAACTATGGAGAAAGCTAGCAAGACATGTCGGAAA 214  
 Db 87 AGAAATTCGCGACTGTGGAGAAGTCGACTATGTGAGAAAGCTAGCAAGACATGTCGGCAA 146  
 Qy 215 CTGTGGCAATCGGGCATTTGTGACACACATGTAAATCATGGAGGGTGCGCCATGG 274  
 Db 147 CTGTGGCAACCGGACACTGTGACGACAGTCGTAAGTCGGAGACTSGAGCCATGG 206  
 Qy 275 ACCGTCGATGTCGTTAACGGAAACACATGTGTTCTGTACTTCATGTAAAGAGC 334  
 Db 207 TCGTGTCAATGTCGTTAACACATGTGCTGACTTCATGTAAAGAGC 266  
 Qy 335 CGAAAAGCTTGTCAGACACAACATTAAAGCGAAACACTCGCTCAAGACAAACCTTAATG 393  
 Db 267 CGAAAAGCTTGCCAGAACGCTCACGTCGAAAGAAATTCGGCCTGATGACGTTAAAG 325

Search completed: March 18, 2005, 13:52:15  
 Job time : 388 secs

Post-processing: Maximum Match 0% Listing first 45 summaries									
SUMMARIES									
Result No.	Score	Query	Match	Length	DB	ID	Description		
1	154.2	34.6	565	4	US-09-589-733C-6		Sequence 6, Appli		
2	99.4	22.3	150	1	US-08-377-687-31		Sequence 31, Appli		
3	99.4	22.3	150	1	US-08-777-192-31		Sequence 31, Appli		
4	99.4	20.5	150	1	US-08-377-687-33		Sequence 33, Appli		
5	91.4	20.5	150	3	US-08-777-192-33		Sequence 33, Appli		
6	91.4	20.5	150	3	US-08-971-982-33		Sequence 33, Appli		
7	86.6	19.4	150	1	US-08-377-687-34		Sequence 34, Appli		
8	86.6	19.4	150	1	US-08-777-192-34		Sequence 34, Appli		
9	86.6	19.4	150	3	US-08-971-982-34		Sequence 34, Appli		
10	86.6	19.4	150	3	US-08-377-687-35		Sequence 36, Appli		
11	58.4	13.1	147	1	US-08-777-192-35		Sequence 36, Appli		
12	58.4	13.1	147	1	US-08-971-982-35		Sequence 36, Appli		
13	58.4	13.1	147	3	US-08-971-982-36		Sequence 36, Appli		
14	44.6	10.0	270	1	US-08-377-687-34		Sequence 14, Appli		
15	44.6	10.0	270	3	US-08-777-192-34		Sequence 14, Appli		
16	44.6	10.0	270	4	US-09-829-381D-14		Sequence 14, Appli		
17	44.6	10.0	286	3	US-08-627-706-12		Sequence 12, Appli		
18	44.6	10.0	286	3	US-08-103-489-12		Sequence 12, Appli		
19	44.6	10.0	286	4	US-09-829-381D-12		Sequence 12, Appli		
20	40.8	9.1	500	1	US-08-627-706-9		Sequence 9, Appli		
21	40.8	9.1	500	3	US-09-103-489-9		Sequence 9, Appli		
22	40.8	9.1	500	4	US-09-829-381D-9		Sequence 9, Appli		
23	40.0	9.0	414	1	US-08-777-192-48		Sequence 48, Appli		
24	40.0	9.0	414	3	US-08-971-982-48		Sequence 48, Appli		
25	40.0	9.0	414	3	US-09-949-016-11789		Sequence 19, Appli		
26	40.0	9.0	414	4	US-09-077-948A-19		Sequence 45, Appli		
27	40.0	9.0	414	4	US-09-949-016-11789		Sequence 45, Appli		

RESULT 2  
US-08-377-687-31  
; Sequence 31, Application US/08377687  
; Patent No. 5538525

GENERAL INFORMATION:  
 ; APPLICANT: BROEKERT, WILLEM F.  
 ; APPLICANT: CANNUE, BRUNO P.A.  
 ; APPLICANT: OSBORN, RUPERT W.  
 ; APPLICANT: REES, SARAH B.  
 ; APPLICANT: TERRAS, FRANKY R.G.  
 ; APPLICANT: VANDERLEYDEN, JOZEF  
 TITLE OF INVENTION: BIOCIDAL PROTEINS  
 NUMBER OF SEQUENCES: 59

CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN  
 STREET: 1100 NEW YORK AVENUE, N.W.  
 CITY: WASHINGTON  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20005

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/377,687  
 FILING DATE: 2005  
 CLASSIFICATION:  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 08/002,480  
 FILING DATE: 04-JAN-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: KOKULIS, PAUL N.  
 REGISTRATION NUMBER: 16,773  
 REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A  
 TELECOMMUNICATION INFORMATION:  
 LENGTH: 150 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: both  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 US-08-377-192-31

Query Match 22.3%; Score 99.4; DB 1; Length 150;  
 Best Local Similarity 79.2%; Pred. No. 4.6e-21;  
 Matches 118; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

Qy 177 GAACTATGCGAAGAAAGCTTACGGAGGTGGCAATACGGGACATTGT 236  
 Db 1 GAGCTTGCGGAAGGGTTCTAGACTTGGCTGGAACATCTGGTGC 60

Qy 237 GACAACCAATGTAATCATGGAGGGTGGGCCATGGAGCTGTCACTGGTAACGGG 296  
 Db 61 GATAACCAATGAACTGGCTTGGAGGGTGTGCACTGGTAAACGGA 120

Query Match 22.3%; Score 99.4; DB 1; Length 150;  
 Best Local Similarity 79.2%; Pred. No. 4.6e-21;  
 Matches 118; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

Qy 237 GAACTATGCGAAGAAAGCTTACGGAGGTGGCAATACGGGACATTGT 325  
 Db 121 AAGCATATGCTTCGCTACTTCACTG 149

RESULT 4  
US-08-377-687-31  
; Sequence 31, Application US/08377687  
; Patent No. 5538525

GENERAL INFORMATION:  
 ; APPLICANT: BROEKERT, WILLEM F.  
 ; APPLICANT: CANNUE, BRUNO P.A.  
 ; APPLICANT: OSBORN, RUPERT W.  
 ; APPLICANT: REES, SARAH B.  
 ; APPLICANT: TERRAS, FRANKY R.G.  
 ; APPLICANT: VANDERLEYDEN, JOZEF  
 TITLE OF INVENTION: BIOCIDAL PROTEINS  
 NUMBER OF SEQUENCES: 59  
 CORRESPONDENCE ADDRESS:  
 ; Sequence 31, Application US/08377687  
 ; Patent No. 5824869

GENERAL INFORMATION:  
 ; APPLICANT: BROEKERT, WILLEM F.  
 ; APPLICANT: CANNUE, BRUNO P.A.  
 ; APPLICANT: OSBORN, RUPERT W.  
 ; APPLICANT: REES, SARAH B.  
 ; APPLICANT: TERRAS, FRANKY R.G.  
 ; APPLICANT: VANDERLEYDEN, JOZEF  
 TITLE OF INVENTION: BIOCIDAL PROTEINS  
 NUMBER OF SEQUENCES: 59  
 CORRESPONDENCE ADDRESS:

ADDRESS/B: CUSHMAN DARBY & CUSHMAN  
STREET: 1100 NEW YORK AVENUE, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/971,982  
FILING DATE: 17-NO- 6187904-1997  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/002,480  
FILING DATE: 04-JAN-1993

ATTORNEY/AGENT INFORMATION:  
NAME: KOKULIS, PAUL N.  
REGISTRATION NUMBER: 16,773  
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-861-3000  
TELEFAX: 202-822-0944

INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 150 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 31:  
US-08-971-982-31

Query Match 22.3%; Score 99.4; DB 3; Length 150;  
Best Local Similarity 79.2%; Pred. No. 4.6e-2;  
Matches 118; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

Qy 177 GAACTATGGAGAAGTGTAGAGCATGTTGGGAAACTGGGCATAACGGACATTG 236  
Db 1 GAGCTTTCGGAGAGGGCTCTAACGTTGAGCTGGCTTGAGCTGAGCTTGAGCTG 149

Qy 237 GACAACATGTTGTTGTTGTTACTCAATTG 325  
Db 61 GATGATCAATTGCAATGCACTGGGAACTGGAACTGGGAAACATGGACATTG 60

Qy 297 AAACACATGTTGTTGTTGTTACTCAATTG 325  
Db 121 AAGCATATGTTGCTTCAGCTCACTTCAGCT 149

RESULT 6  
US-08-77-192-33  
Sequence 33, Application US/08777192  
Patent No. 5624869

GENERAL INFORMATION:  
APPLICANT: BROEKERT, WILLEM F.  
APPLICANT: CAMMIE, BRUNO P.A.  
APPLICANT: OSBORN, RUPERT W.  
APPLICANT: REES, SARAH B.  
APPLICANT: TERRAS, FRANKY R.G.  
APPLICANT: VANDERLEIDEN, JOZEF  
TITLE OF INVENTION: BIOCIDAL PROTEINS  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CUSHMAN DARBY & CUSHMAN  
STREET: 1100 NEW YORK AVENUE, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005

RESULT 5  
US-08-377-687-33  
Sequence No. 33, Application US/08377687  
Patent No. 5538525

GENERAL INFORMATION:  
APPLICANT: BROEKERT, WILLEM F.  
APPLICANT: CAMMIE, BRUNO P.A.  
APPLICANT: OSBORN, RUPERT W.  
APPLICANT: REES, SARAH B.  
APPLICANT: TERRAS, FRANKY R.G.  
APPLICANT: VANDERLEIDEN, JOZEF  
TITLE OF INVENTION: BIOCIDAL PROTEINS  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CUSHMAN DARBY & CUSHMAN  
STREET: 1100 NEW YORK AVENUE, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/377,687

FILING DATE:  
CLASSIFICATION: 800  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/002,480  
FILING DATE: 04-JAN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: KOKULIS, PAUL N.  
REGISTRATION NUMBER: 16,773  
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-861-3000  
TELEFAX: 202-822-0944

INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 150 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-377-687-33

Query Match 20.5%; Score 91.4; DB 1;  
Best Local Similarity 75.8%; Pred. No. 1.4e-18;  
Matches 113; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

Qy 177 GAACTATGGAGAAGTGTAGAGCATGTTGGGAAACTGGGCATAACGGACATTG 236  
Db 1 GAGCTTTCGGAGAGGGCTCTAACGTTGAGCTGGCTTGAGCTGAGCTTGAGCTG 60

Qy 237 GACAACATGTTGTTGTTGTTACTCAATTG 325  
Db 61 GATGATCAATTGCAATGCACTGGGAACTGGGAACTGGGAAACATGGACATTG 120

Qy 297 AAACACATGTTGTTGTTGTTACTCAATTG 325  
Db 121 AAGCATATGTTGCTTCAGCTCACTTCAGCT 149

RESULT 6  
US-08-77-192-33  
Sequence 33, Application US/08777192  
Patent No. 5624869

GENERAL INFORMATION:  
APPLICANT: BROEKERT, WILLEM F.  
APPLICANT: CAMMIE, BRUNO P.A.  
APPLICANT: OSBORN, RUPERT W.  
APPLICANT: REES, SARAH B.  
APPLICANT: TERRAS, FRANKY R.G.  
APPLICANT: VANDERLEIDEN, JOZEF  
TITLE OF INVENTION: BIOCIDAL PROTEINS  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CUSHMAN DARBY & CUSHMAN  
STREET: 1100 NEW YORK AVENUE, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/777,192  
FILING DATE:  
CLASSIFICATION:

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/002,480  
 FILING DATE: 04-JAN-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: KOKULIS, PAUL N.  
 REGISTRATION NUMBER: 16,773  
 REFERENCE/DOCKET NUMBER: 99042/SEE .36525/US/A  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-861-3000  
 TELEX/FAX: 202-822-0944  
 INFORMATION FOR SEQ ID NO: 33:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 150 base pairs  
 STRANDBENDNESS: both  
 TYPE: nucleic acid  
 TOPOLogy: linear  
 MOLECULE TYPE: cDNA  
 US-08-777-192-33

Query Match 20.5%; Score 91.4; DB 3; Length 150;  
 Best Local Similarity 75.8%; Prod. No. 1.4e-18;  
 Matches 113; Conservative 0; Mismatches 0; Gaps 0;

Qy 177 GACATATGGAAAGCTAGCAAGCATGGCAATACGGGACATTGT 236  
 Db 1 GAGCTTGCGAAGCCTTAAGCTGTCTGAAACACTAACGATTCG 60

Query Match 20.5%; Score 91.4; DB 1; Length 150;  
 Best Local Similarity 75.8%; Prod. No. 1.4e-18;  
 Matches 113; Conservative 0; Mismatches 0; Gaps 0;

Qy 177 GACATATGGAAAGCTAGCAAGCATGGCAATACGGGACATTGT 236  
 Db 1 GAGCTTGCGAAGCCTTAAGCTGTCTGAAACACTAACGATTCG 60

Qy 237 GACATATGGAAAGCTAGCAAGCATGGCAATACGGGACATTGT 296  
 Db 61 GATGTCATGCAACTCTGGAGGAGCTGTGCTGTGAGCTTGA 120

Qy 297 AAACATATGGTTCTGTACTTCAATTG 325  
 Db 121 AAGCTATGCTCTGTACTTCAATTG 149

RESULT 8  
 US-08-377-687-34  
 ; Sequence 34, Application US/08377687  
 ; Patent No. 5538555

GENERAL INFORMATION:  
 APPLICANT: BROEKERT, WILLEM F.  
 CARRMUE, BRUNO P.A.  
 OSBORN, RUPERT W.  
 REES, SARAH B.  
 APPLICANT: VANDERLEYDEN, JOZEF  
 TITL OF INVENTION: BIOCIDAL PROTEINS  
 NUMBER OF SEQUENCES: 59  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: CUSHMAN DARBY & CUSHMAN  
 STREET: 110 NEW YORK AVENUE, N.W.  
 CITY: WASHINGTON D.C.  
 STATE: D.C.  
 ZIP: 20005  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/971,982  
 FILING DATE: 17-Mar-1997  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/002,480  
 FILING DATE: 04-JAN-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: KOKULIS, PAUL N.  
 REGISTRATION NUMBER: 16,773  
 REFERENCE/DOCKET NUMBER: 99042/SEE .36525/US/A  
 TELECOMMUNICATION INFORMATION:

TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 US-08-377-887-34

Query Match 19.4% ; Score 86.6 ; DB 1; Length 150;  
 Best Local Similarity 73.8%; Pred. No. 4.3e-17; Indels 0; Gaps 0;  
 Matches 110; Conservative 0; Mismatches 39;

Qy 177 GAACTATCGAGAAGCTAGCAAGCATGGGAAACTGTGGCAATACGGACATTGT 236  
 Db 1 GAGCTTTCGGAGAAGGCTTCAAGACTGGAAACTAGCATGGATCTGC 60

Qy 177 GAACTATCGAGAAGCTAGCAAGCATGGGAAACTGTGGCAATACGGACATTGT 236  
 Db 1 GAGCTTTCGGAGAAGGCTTCAAGACTGGAAACTAGCATGGATCTGC 60

Qy 237 GAAACCATTGTAATCTGGAGGGCCATGGAGCTGTGGTAACGG 296  
 Db 61 GATAAACAGTGCAAGTCAGTCTAGACTGGAAACACTAAGCATGGT 60

Qy 297 AAACACATGTGTTCTGTTACTICAATG 325  
 Db 121 AAGCATATGCTCTCTACTCAACTG 149

RESULT 10  
 US-08-971-982-34  
 Sequence 34, Application US/08971982  
 Patent No. 6187904

GENERAL INFORMATION:  
 APPLICANT: BROEKERT, WILLEM F.  
 ADDRESS: CUSHMAN, DARBY & CUSHMAN  
 STREET: 1100 NEW YORK AVENUE, N.W.  
 CITY: WASHINGTON  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20005  
 COMPUTER READABLE FORM:  
 NUMBER OF SEQUENCES: 59  
 CORRESPONDENCE ADDRESS:  
 APPLICANT: CAMMUE, BRUNO P.A.  
 APPLICANT: OSBORN, RUPERT W.  
 APPLICANT: REES, SARAH B.  
 APPLICANT: TERRAS, FRANKY R.G.  
 APPLICANT: VANDERLEYDEN, JOZEF  
 TITLE OF INVENTION: BIOCIDAL PROTEINS  
 NUMBER OF SEQUENCES: 59  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: CUSHMAN DARBY & CUSHMAN  
 STREET: 1100 NEW YORK AVENUE, N.W.  
 CITY: WASHINGTON  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20005  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/777,192  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: KOKULIS, PAUL N.  
 REGISTRATION NUMBER: 16,773  
 REFERENCE/DOCKET NUMBER: 99042/SEE.36525/us/a  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-861-3000  
 TELEXFAX: 202-862-0944  
 INFORMATION FOR SEQ ID NO: 34:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: KOKULIS, PAUL N.  
 REGISTRATION NUMBER: 16,773  
 REFERENCE/DOCKET NUMBER: 99042/SEE.36525/us/a  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-861-3000  
 TELEXFAX: 202-822-0944  
 INFORMATION FOR SEQ ID NO: 34:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 150 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: both  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 US-08-777-192-34

Qy 177 GAACTATCGAGAAGCTAGCAAGCATGGGAAACTGTGGCAATACGGACATTGT 236  
 Db 1 GAGCTTTCGGAGAAGGCTTCAAGACTGGAAACTAGCATGGATCTGC 60

Qy 237 GAAACCATTGTAATCTGGAGGGCCATGGAGCTGTGGTAACGG 296  
 Db 61 GATAAACAGTGCAAGTCAGTCTAGACTGGAAACACTAAGCATGGT 60

RESULT 9  
 US-08-777-192-34  
 Sequence 34, Application US/08777192  
 Patent No. 5824869

GENERAL INFORMATION:  
 APPLICANT: BROEKERT, WILLEM F.  
 ADDRESS: CUSHMAN, DARBY & CUSHMAN  
 STREET: 1100 NEW YORK AVENUE, N.W.  
 CITY: WASHINGTON  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20005  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/971,982  
 FILING DATE: 17-Nov-1997  
 CLASSIFICATION: <Unknown>  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 08/002,480  
 ATTORNEY/AGENT INFORMATION:  
 NAME: KOKULIS, PAUL N.  
 REGISTRATION NUMBER: 16,773  
 REFERENCE/DOCKET NUMBER: 99042/SEE.36525/us/a  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-861-3000  
 TELEXFAX: 202-862-0944  
 INFORMATION FOR SEQ ID NO: 34:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 150 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: both  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 US-08-971-982-34

SEQUENCE DESCRIPTION: SEQ ID NO: 34:

Query Match 19.4% ; Score 86.6 ; DB 1; Length 150;  
 Best Local Similarity 73.8%; Pred. No. 4.3e-17; Indels 0; Gaps 0;  
 Matches 110; Conservative 0; Mismatches 39;

Qy 177 GAACTATCGAGAAGCTAGCAAGCATGGGAAACTGTGGCAATACGGACATTGT 236  
 Db 1 GAGCTTTCGGAGAAGGCTTCAAGACTGGAAACTAGCATGGATCTGC 60

```

RESULT 11
US-08-377-687-36
; Sequence 36, Application US/08377687
; Patent No. 5538525
; GENERAL INFORMATION:
; APPLICANT: BROEKERT, WILLEM F.
; APPLICANT: CAMMUE, BRUNO P.A.
; APPLICANT: OSBORN, RUPERT W.
; APPLICANT: REES, SARAH B.
; APPLICANT: TERRAS, FRANCY R.G.
; APPLICANT: VANDERLEDEN, JOZEF
; TITLE OF INVENTION: BIOCIDAL PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/377,687
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/002,480
; FILING DATE: 04-JAN-1993
; ATTORNEY AGENT INFORMATION:
; NAME: KOKULS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 93042/SEE.36525/US/A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 147
; BASE PAIRS:
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-377-687-36

Query 297 AACACATGTTCTGTACTTCAATTG 325
Db 121 AAGCATATGTCTCTGTACTTCAGTG 149

Query 13.1%; Score 58.4%; DB 1; Length 147;
Best Local Similarity 66.9%; Pred. No. 2.5e-18;
Matches 99; Conservative 0; Mismatches 46; Indexes 3; Gaps 1;
Query 178 AACTATGGAGAAAGCTTGGCAAAGACTGGTCCGGAAACTGGCAATACTGGGACATTTGTC 237
Db 2 ACCTTGCGAGAGGGCTCTCTACTGGACTGGAAACTGGCAATACTGGGAACTTGCG 61
Query 238 ACAACCAATGTAATCATGGAGGGGGGGCCATGGAGCTGTGCTAAACGGGA 297
Db 62 ATACCTATGGAGAAACTGGATCTGCCTAACCATGGCTGCTAAAG---AGGGAA 118
Query 298 AACACATGTTCTGTACTTCAATTG 325
Db 119 ACTGGAAAGTGTCTGTCTACTTCGATG 146

```

TITLE OF INVENTION: BIOCIDAL PROTEINS  
 NUMBER OF SEQUENCES: 59  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: CUSHMAN, DARBY & CUSHMAN  
 STREET: 1100 NEW YORK AVENUE, N.W.  
 CITY: WASHINGTON  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20015

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/971,982

FILING DATE: 17-N. 6187904-1997  
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/002,480

FILING DATE: 04-JAN-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: KOKULIS, PAUL N.

REGISTRATION NUMBER: 16,773  
 REFERENCE/DOCKET NUMBER: 99042/SEE .36525/US/A

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-851-3000  
 TELEFAX: 202-822-0944

INFORMATION FOR SEQ ID NO: 36:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 147 base Pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: both  
 TOPOLOGY: linear

MOLECULE TYPE: cDNA  
 SEQUENCE DESCRIPTION: SEQ ID NO: 36:

US-08-971-982-36

Query Match Score 58.4%; DB 3; Length 147;

Best Local Similarity 66.9%; Pred. No. 2.5e-08;  
 Matches 99; Conservative 0; Mismatches 46; Indels 3; Gaps 1;

Db 2 ACCTTTCGAGAGCTCTTACTGGAACTCTGGCAATACGGGACATTGCG 237

Qy 238 ACAACCATGTAATCATGGAGGGTCCGCCATGGCGTGTCACTGGTAACGGA 297

Db 62 ATACTCATGCGAAACTGGGATCTGCATAAG--AGGGAA 118

Qy 298 AACACATGTTCTGTACTTCATTG 325

Db 119 ACTGGAACTGTTCTGTACTCGATG 146

RESULT 14

Sequence 14, Application US/086227706  
 Patent No. 5773696

GENERAL INFORMATION:  
 APPLICANT: Liang, Jihong  
 APPLICANT: Shah, Dilip M.

APPLICANT: Wu, Yonne S.

APPLICANT: Rosenberger, Cindy A.

TITLE OF INVENTION: Antifungal Polypeptide and Methods for

TITLE OF INVENTION: Controlling Plant Pathogenic Fungi

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F  
 STREET: 700 Chesterfield Village Parkway No. 5773696th  
 CITY: St. Louis  
 STATE: Missouri

RESULT 14

Sequence 14, Application US/09103489  
 Patent No. 6215048

GENERAL INFORMATION:

APPLICANT: Liang, Jihong

APPLICANT: Shah, Dilip M.

APPLICANT: Wu, Yonne S.

APPLICANT: Rosenberger, Cindy A.

TITLE OF INVENTION: Antifungal Polypeptide and Methods for

TITLE OF INVENTION: Controlling Plant Pathogenic Fungi

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F  
 STREET: 700 Chesterfield Village Parkway No. 5773696th  
 CITY: St. Louis  
 STATE: Missouri

COUNTRY: USA

ZIP: 63198

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

APPLICATION NUMBER: US/08/627,706

FILING DATE:

CLASSIFICATION: 436

ATTORNEY/AGENT INFORMATION:

NAME: Cohen, Charles E.

REGISTRATION NUMBER: 34,565

REFERENCE/DOCKET NUMBER: 38-21 (10700) A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (314) 537-6724

TELEFAX: (314) 537-6047

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 270 base Pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: 1-linear

MOLECULE TYPE: cDNA

US-08-627-706-14

Query Match Score 10.0%; DB 1; Length 270;

Best Local Similarity 53.8%; Pred. No. 0.00065;  
 Matches 92; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

Qy 163 CATCCGTTAGTGCGAAACTGCGAGAACATGGCAAGACATGGTGGAAACTGTCGGAAACTGTCGGCA 222

Db 95 CAATGGGACATGGATGCAAGCTGGCGAGAACATGGTGGAACTGTCGGTTGGTGGAA 154

Qy 223 ATACGGGACATTTGCGACAACCAATGTAATCATGGGAGGGTGGGCCATGGAGGGTGGTC 282

Db 155 ACAACAAATGCGAGAACCAATGCGAAACCATGCGAAACCTGAAAGGGAAACACGGATCTGCA 214

RESULT 15

US-09-103-489-14

Sequence 14, Application US/09103489

Patent No. 6215048

GENERAL INFORMATION:

APPLICANT: Liang, Jihong

APPLICANT: Shah, Dilip M.

APPLICANT: Wu, Yonne S.

APPLICANT: Rosenberger, Cindy A.

TITLE OF INVENTION: Antifungal Polypeptide and Methods for

TITLE OF INVENTION: Controlling Plant Pathogenic Fungi

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F  
 STREET: 700 Chesterfield Village Parkway No. 6215048th

CITY: St. Louis

STATE: Missouri

COUNTRY: USA

ZIP: 63198

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/103,489

FILING DATE: 24-JUN-1998

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

| NAME: Cohen, Charles E.  
| REFERENCE DOCKET NUMBER: 34,565  
| TELECOMMUNICATION INFORMATION:  
| TELEPHONE: (314) 537-6224  
| TELEFAX: (314) 537-6047  
| INFORMATION FOR SEQ ID NO: 14:  
| SEQUENCE CHARACTERISTICS:  
| LENGTH: 270 base pairs  
| TYPE: nucleic acid  
| STRANDEDNESS: single  
| TOPOLOGY: linear  
| MOLECULE TYPE: cDNA  
us-09-103-489-14

Query Match 10.0% Score 44.6; DB 3; Length 270;  
Best Local Similarity 53.8%; Pred. No. 0.00055;  
Matches 92; Conservative 0; Mismatches 79; Indels 0; Gaps 0;  
Qy 163 CATCCGTTAGTGAGAACTATCGAGAAGTAGCTGGAAACTGTGCA 222  
Db 95 CAAATGGTGGATCCAAGTTGTGCGAGGACCAAGTGGACATGGTAGGAGTTGGGA 154  
Qy 223 ATACGGGACATTGTGACAACCATGTAATCATGGGAGGGTGGCCCATGGCCTGTC 282  
Db 155 ACAACAATGCAATGCAGAACCATGCAAGAACCTGAAAGGCCAACACGATCTTCA 214  
Qy 283 ATGTGCCTAACCGGAAACACATGTGTTCTGTACTTCATTGTAAAAAAG 333  
Db 215 ACTATGTTCCCAAGTCACAAATGTTGTTACTTCATGTTAATAG 265

Search completed: March 18, 2005, 16:31:56  
Job time : 137 secs

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OM nucleic - nucleic search, using SW model

Run on: March 18, 2005, 14:31:06 ; Search time 420 Seconds  
(without alignments)

6321.756 Million cell updates/sec

Title: US-09-763-019-5

Perfect score: 446

Sequence: 1 atggtaatcggttgttc.....ttccaaacgttgc.....

Scoring table: IDENTITY\_NUC

Gapop 10\_0 , Gapext 1.0

Searched: 5544816 seqs, 2976611598 residues

Total number of hits satisfying chosen parameters: 11089632

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:\*

1: /cgn2\_6/\_ptodata/2/pubnra/BCT/US07\_PUBCOMB.seq:\*

2: /cgn2\_6/\_ptodata/2/pubnra/BCT/NEW\_PUB.seq:\*

3: /cgn2\_6/\_ptodata/2/pubnra/US06\_NEWPUB.seq:\*

4: /cgn2\_5/\_ptodata/2/pubnra/US07\_PUBCOMB.seq:\*

5: /cgn2\_6/\_ptodata/2/pubnra/PCTUS\_PUBCOMB.seq:\*

6: /cgn2\_6/\_ptodata/2/pubnra/US07\_NEWPUB.seq:\*

7: /cgn2\_6/\_ptodata/2/pubnra/US8\_NEWPUB.seq:\*

8: /cgn2\_6/\_ptodata/2/pubnra/US09\_PUBCOMB.seq:\*

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10: /cgn2\_6/\_ptodata/2/pubnra/US09B\_PUBCOMB.seq:\*

11: /cgn2\_6/\_ptodata/2/pubnra/US09C\_PUBCOMB.seq:\*

12: /cgn2\_6/\_ptodata/2/pubnra/US09\_NEWPUB.seq:\*

13: /cgn2\_6/\_ptodata/2/pubnra/US10\_PUBCOMB.seq:\*

14: /cgn2\_6/\_ptodata/2/pubnra/US10B\_PUBCOMB.seq:\*

15: /cgn2\_6/\_ptodata/2/pubnra/US10C\_PUBCOMB.seq:\*

16: /cgn2\_6/\_ptodata/2/pubnra/US10D\_PUBCOMB.seq:\*

17: /cgn2\_6/\_ptodata/2/pubnra/US10E\_PUBCOMB.seq:\*

18: /cgn2\_6/\_ptodata/2/pubnra/US10F\_PUBCOMB.seq:\*

19: /cgn2\_6/\_ptodata/2/pubnra/US10\_NEWPUB.seq:\*

20: /cgn2\_6/\_ptodata/2/pubnra/US11\_NEWPUB.seq:\*

21: /cgn2\_6/\_ptodata/2/pubnra/US60\_NEWPUB.seq:\*

22: /cgn2\_6/\_ptodata/2/pubnra/US60\_PUBCOMB.seq:\*

RESULT 1

US-10-178-449A-48

; Sequence 48, Appl

; Sequence 31, Appl

; Sequence 3, Appl

; Sequence 1, Appl

; Sequence 13, Appl

; Sequence 9, Appl

; Sequence 11, Appl

; Sequence 21, Appl

; Sequence 17, Appl

; Sequence 6, Appl

; Sequence 19, Appl

; Sequence 23, Appl

; Sequence 15, Appl

; Sequence 31, Appl

; Sequence 33, Appl

; Sequence 29, Appl

; Sequence 7, Appl

; Sequence 34, Appl

; Sequence 34, Appl

; Sequence 5, Appl

; Sequence 36, Appl

; Sequence 283, Appl

; Sequence 36, Appl

; Sequence 88, Appl

; Sequence 25, Appl

; Sequence 27, Appl

; Sequence 14, Appl

; Sequence 14, Appl

; Sequence 12, Appl

; Sequence 12, Appl

; Sequence 21, Appl

; Sequence 15, Appl

; Sequence 9, Appl

; Sequence 9, Appl

; Sequence 9, Appl

; Sequence 2046, Appl

; Sequence 46, Appl

; Sequence 19, Appl

; Sequence 45, Appl

; Sequence 2, Appl

; Sequence 3, Appl

; Sequence 1, Appl

; Sequence 58, Appl

## ALIGNMENTS

ALIGNS

1: Sequence 48, Application US/10176449A

2: Publication No. US20030140368A1

3: GENERAL INFORMATION:

4: APPLICANT: Famodu, Omolayo O.

5: APPLICANT: Herrmann, Rafael

6: APPLICANT: Lu, Albert L.

7: APPLICANT: McCurchen, Billy Fred

8: APPLICANT: Miao, Guo-Hua

9: APPLICANT: Presnail, James K.

10: APPLICANT: Rafalski, Jan Antoni

11: APPLICANT: Wong, Zude

12: TITLE OF INVENTION: Plant Defensins

13: FILE REFERENCE: 35718/249123

14: CURRENT APPLICATION NUMBER: US/10/178-449A

15: CURRENT FILING DATE: 2002-06-21

16: PRIOR APPLICATION NUMBER: US 10/030,516

17: PRIOR FILING DATE: 2000-05-03

18: NUMBER OF SEQ ID NOS: 51

19: SOFTWARE: FastSEQ for Windows Version 4.0

20: SEQ ID NO 48

21: LENGTH: 529

22: TYPE: DNA

23: ORGANISM: Vernonia mespilifolia

24: FEATURE: NAME/KEY: misc\_feature

25: LOCATION: 480, 515, 521, 529

26: OTHER INFORMATION: n = A,T,C or G

27: FEATURE:

\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	209.4	47.0	529	15	US-10-178-449A-48
2	203	45.5	579	15	US-10-178-449A-31
3	168.6	37.8	460	15	US-10-178-449A-3
4	168.6	37.8	503	15	US-10-178-449A-1
5	161	36.1	461	15	US-10-178-449A-46
6	156.4	35.1	457	15	US-10-178-449A-13
7	156.4	35.1	463	15	US-10-178-449A-9
8	156.4	35.1	603	15	US-10-178-449A-11
9	154.8	34.7	458	15	US-10-178-449A-21
10	154.8	34.7	460	15	US-10-178-449A-17
11	154.6	34.6	565	17	US-10-636-396-6

NAME / KEY : CDS  
LOCATION : (25) . . . (372)  
US-10-178-449A-48

Query Match 47.0%; Score 209; DB 15; Length 529;  
Best Local Similarity 82.5%; Pred. No. 4.2e-48;  
Matches 240; Conservative 51; Indels 0; Gaps 0;

Db 155 AGATATCGCATCCGTTAGTGAGAACTATGGAGAAAGCTAGCAAGACATGTGAAACTTAATGC 394  
Db 78 AGAAATCTCGTGTGAGCTGAGCTTGGAGAAAGCTAGCAAGACATGTGAAACTTAATGC 445  
Db 212 AGCTTGTCTATGTTGGGGAAAACATGTGTTTCATTTCAATTGTAAAAAGC 271

Qy 335 CGAAAAGCTTGTCTAAGACAACATTAAGCCGAAACTCAGCTCAAGACAACATTAATGTC 394  
Db 272 TGAAAACCTCGTCAAGATAAGCTTAAAGCTGAGCTTGGAGAAACTCAAGGC 331  
Db 395 CCAAAGCTTGTACGGTGTGCCAGAAGTGGTCAAGACGTGACATCC 445  
Db 332 AGATAAGTTGACCATGTGCAAAAGAGTAGTACAATGTGAACTGC 382

RESULT 3  
US-10-178-449A-3  
Sequence 3, Application US/10178449A  
Publication No. US20030140368A1  
GENERAL INFORMATION:  
APPLICANT: Famodu, Omolayo O.  
APPLICANT: Herrmann, Rafael L.  
APPLICANT: Lu, Albert L.  
APPLICANT: McCurthen, Billy Fred  
APPLICANT: Miao, Guo-Hua  
APPLICANT: Presnail, James K.  
APPLICANT: Ratajski, Jan Antoni  
APPLICANT: Wang, Zude  
TITLE OF INVENTION: Plant Defensins  
FILE REFERENCE: 35718/249123  
CURRENT APPLICATION NUMBER: US/10/178-449A  
CURRENT FILING DATE: 2002-06-21  
PRIOR APPLICATION NUMBER: US 10/030,516  
PRIOR FILING DATE: 2000-05-03  
PRIOR APPLICATION NUMBER: PCT/US00/11952  
PRIOR FILING DATE: 2000-05-03  
PRIOR APPLICATION NUMBER: US 60/133,039  
PRIOR FILING DATE: 1999-05-07  
NUMBER OF SEQ ID NOS: 51  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 3  
LENGTH: 460  
TYPE: DNA  
ORGANISM: Dimorphotheca sinuata  
US-10-178-449A-3

Query Match 37.8%; Score 168; DB 15; Length 460;  
Best Local Similarity 81.6%; Pred. No. 1e-36;  
Matches 195; Conservative 0; Mismatches 44; Indels 0;  
Qy 155 AGATATGGCATCGTGTAGTGGAGAACTATGGAGAAAGCTAGCAAGACATGTGAAACTTAATGC 214  
Db 87 AGAAATGGCATCGTGTAGTGGAGAAAGCTAGCAAGACATGTGAAACTTAATGC 214  
Db 215 CTGTGGCAATACGGACATGTGACAACCAATGAACTATGGAGGTGGCCCATGG 274  
Db 152 CTGTGGCAACACGGACATGTGCAATACTGTGAACTGTGACATGG 211  
Db 275 AGCTTGTCTATGTTGGAGAAACATTAAGCCGAAACTCTCAAGACAACATTAATGTC 334  
Db 92 AGAAATCTCGATCGTGTGAGCTGAGCTACAGATGTCATGG 151  
Db 207 TCGTGTCTATGTCGGTGTGCCAAAGACATGTGCTCATGTCATGG 266  
Db 335 CGAAAGCTTCTCTAGACAAACTTAAGCCGAAACACTCTCAAGACAACATTAATGTC 393  
Db 267 CGAAAAGCTTGGCCAGACAGCTPACGTGCTGAAAAAATTGGCCGTACGCTGAAACTTAATGTC 325

RESULT 4  
US-10-178-449A-1  
Sequence 1, Application US/10178449A  
Publication No. US20030140368A1  
GENERAL INFORMATION:  
APPLICANT: Famodu, Omolayo O.  
APPLICANT: Herrmann, Rafael L.  
APPLICANT: Lu, Albert L.  
APPLICANT: McCurthen, Billy Fred  
APPLICANT: Presnail, James K.  
APPLICANT: Ratajski, Jan Antoni  
APPLICANT: Wang, Zude  
TITLE OF INVENTION: Plant Defensins  
FILE REFERENCE: 35718/249123  
CURRENT APPLICATION NUMBER: US/10/178-449A  
CURRENT FILING DATE: 2002-06-21  
PRIOR APPLICATION NUMBER: PCT/US00/11952  
PRIOR FILING DATE: 2000-05-03  
PRIOR APPLICATION NUMBER: US 10/030,516  
PRIOR FILING DATE: 2000-05-03  
NUMBER OF SEQ ID NOS: 51  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 3  
LENGTH: 579  
TYPE: DNA  
ORGANISM: Vernonia mepillifolia  
US-10-178-449A-31

Query Match 45.5%; Score 203; DB 15; Length 579;  
Best Local Similarity 81.1%; Pred. No. 2.7e-46;  
Matches 236; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

Qy 155 AGATATGGCATCGTGTAGTGGAGAACTATGGAGAAAGCTAGCAAGACATGTGAAACTTAATGC 214  
Db 207 TCGTGTCTATGTCGGTGTGCCAAAGACATGTGCTCATGTCATGG 266  
Db 335 CGAAAGCTTCTCTAGACAAACTTAAGCCGAAACACTCTCAAGACAACATTAATGTC 393  
Db 267 CGAAAAGCTTGGCCAGACAGCTPACGTGCTGAAAAAATTGGCCGTACGCTGAAACTTAATGTC 325

APPLICANT: Miao, Guo-Hua  
 APPLICANT: Presnail, James K.  
 APPLICANT: Rafalski, Jan Antoni  
 APPLICANT: Weng, Zude  
 TITLE OF INVENTION: Plant Defensins  
 FILE REFERENCE: 35718/249123  
 CURRENT FILING DATE: 2002-06-21  
 PRIOR APPLICATION NUMBER: US 10/030,516  
 PRIOR FILING DATE: 2000-05-03  
 PCT/US00/11952  
 PRIOR APPLICATION NUMBER: PCT/US00/11952  
 PRIOR FILING DATE: 2000-05-03  
 PCT/US00/11952  
 PRIOR FILING DATE: 2000-05-03  
 NUMBER OF SEQ ID NOS: 51  
 SOFTWARE: PastSEQ for Windows Version 4.0  
 SEQ ID NO: 1  
 LENGTH: 503  
 TYPE: DNA  
 ORGANISM: Dimorphotheca sinuata  
 FEATURE: misc\_feature  
 LOCATION: 321, 349, 416, 458, 474, 479, 482, 502  
 OTHER INFORMATION: n = A,T,C or G  
 US-10-178-449A-1

Query Match Score 16.6; DB 15; Length 503;  
 Best Local Similarity 81.6%; Pred. No. 1.1e-36;  
 Matches 195; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

Qy 155 AGATATCGCATCGTTAGTGGAAACTATGCCAGAACGCTGGAA 214  
 Db 80 AGAATCGGACTGTGGAAGTCATACTGGCAATGCTGGAA 139

RESULT 5  
 US-10-178-449A-46  
 Sequence 46, Application US/10178449A  
 Publication No. US20030140368A1  
 GENERAL INFORMATION:  
 APPLICANT: Famodu, Omolayo O.  
 APPLICANT: Herrmann, Rafael  
 APPLICANT: Lu, Albert L.  
 APPLICANT: McCutchen, Billy Fred  
 APPLICANT: Presnail, James K.  
 APPLICANT: Rafalski, Jan Antoni  
 APPLICANT: Weng, Zude  
 TITLE OF INVENTION: Plant Defensins  
 FILE REFERENCE: 35718/249123  
 CURRENT FILING DATE: 2002-06-21  
 PRIOR APPLICATION NUMBER: US 10/030,516  
 PRIOR FILING DATE: 2000-05-03  
 PCT/US00/11952  
 PRIOR APPLICATION NUMBER: PCT/US00/11952  
 PRIOR FILING DATE: 2000-05-03  
 PCT/US00/11952  
 PRIOR FILING DATE: 1999-05-07  
 NUMBER OF SEQ ID NOS: 51  
 SOFTWARE: PastSEQ for Windows Version 4.0  
 SEQ ID NO: 46

Query Match Score 161; DB 15; Length 461;  
 Best Local Similarity 77.9%; Pred. No. 1.4e-34;  
 Matches 194; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

Qy 155 AGATATCGCATCGTTAGTGGAAACTATGCCAGAACGCTGGAA 214  
 Db 76 AGAAATCGGATCCGGTGAAGGAGATTGAGGGCAGAACGATGGCGAAA 135

Query Match Score 36.1%; DB 15; Length 461;  
 Best Local Similarity 77.9%; Pred. No. 1.4e-34;  
 Matches 194; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

Qy 215 CTGTCGAAATACGGACATTGTGACAACTATGCCAGAACGCTGGCGCCATGG 274  
 Db 136 ATGGGAACAAAGCACATGGAACGACTGTGGCAAGTGCAGCTGGCGCCATGG 195

Query Match Score 36.1%; DB 15; Length 461;  
 Best Local Similarity 77.9%; Pred. No. 1.4e-34;  
 Matches 194; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

Qy 275 AGCGTCATCTGCTAACCGGAAACACATCTGTTCTGTTACTCTCAATTGTA 334  
 Db 196 AGCTTCACGTGCGCGTGAAACATCTGCTACTCTCAACTGTCACAGTC 255

Query Match Score 36.1%; DB 15; Length 461;  
 Best Local Similarity 77.9%; Pred. No. 1.4e-34;  
 Matches 194; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

Qy 335 CGAAAGCTTGTCAAGACAACAACTTAAGCGAACACTCTGCTCAAGACAACACTTGTCA 394  
 Db 256 CGAGAAGTTGGCTCAGATAAACTCATAGCAGAAGCTGCTGCAAGAGATGAGC 315

RESULT 6  
 US-10-178-449A-13  
 Sequence 13, Application US/10178449A  
 Publication No. US20030140368A1  
 GENERAL INFORMATION:  
 APPLICANT: Famodu, Omolayo O.  
 APPLICANT: Herrmann, Rafael  
 APPLICANT: Lu, Albert L.  
 APPLICANT: McCutchen, Billy Fred  
 APPLICANT: Miao, Guo-Hua  
 APPLICANT: Presnail, James K.  
 APPLICANT: Rafalski, Jan Antoni  
 APPLICANT: Weng, Zude  
 TITLE OF INVENTION: Plant Defensins  
 FILE REFERENCE: 35718/249123  
 CURRENT FILING DATE: 2002-06-21  
 PRIOR APPLICATION NUMBER: US 10/030,516  
 PRIOR FILING DATE: 2000-05-03  
 PCT/US00/11952  
 PRIOR APPLICATION NUMBER: PCT/US00/11952  
 PRIOR FILING DATE: 2000-05-03  
 PCT/US00/11952  
 PRIOR FILING DATE: 1999-05-07  
 NUMBER OF SEQ ID NOS: 51  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO: 13  
 LENGTH: 457  
 TYPE: DNA  
 ORGANISM: Parthenium argentatum Grey  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: 424, 436  
 OTHER INFORMATION: n = A,T,C or G  
 US-10-178-449A-13

Query Match Score 35.1%; DB 15; Length 457;  
 Best Local Similarity 77.2%; Pred. No. 2.6e-33;  
 Matches 190; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

Qy 155 AGATATCGCATCGTTAGTGGAAACTATGCCAGAACGCTGGCGCCATGGCGAAA 214

Db 91 AGAAATCGATACTGGAGAACATATGTGAAGCAAGAACATGGAA 150  
 Qy 215 CTGTCGCAATAACGGGACTTGTGACAACCAATTAAATCATGGAGGGTGCGCCATGG 274  
 Db 151 TTGTTGTAACACAGACTTGACGACAAATGCGTGCAGCCATGG 210  
 Qy 275 AGCGTGTATGTGGTAACGGGAAACAGATGTGTTCTTACTCAATTGTAAGGC 334  
 Db 211 AGCTTGTCATGTGTCGCTGGGAAACACATGTCCTTGTGACTTCAGTGC 270  
 Qy 335 CGAAAAGCTGTGTCAGCAGAAACTTAAAGCCGAAACACTCGCTCAAGAACAACTTAATGC 394  
 Db 271 CGAGAAGTGGCCAGGTTAACCTCGAGCTGAGAACATTGCAAGGAAGGC 330  
 Qy 395 CCAAA 400  
 Db 331 TGAAA 339

**RESULT 7**  
 US-10-178-449A-9  
 Sequence 9, Application US/10178449A  
 Publication No. US20030140368A1  
 GENERAL INFORMATION  
 APPLICANT: Famodu, Omolayo O.  
 APPLICANT: Herrmann, Rafael L.  
 APPLICANT: Lu, Albert L.  
 APPLICANT: McCutchen, Billy Fred  
 APPLICANT: Miao, Guo-Hua  
 APPLICANT: Presnail, James K.  
 APPLICANT: Rafalski, Jan Antoni  
 APPLICANT: Weng, Zude  
 TITLE OF INVENTION: Plant Defensins  
 FILE REFERENCE: 35718/249123  
 CURRENT FILING DATE: 2002-05-03  
 PRIOR APPLICATION NUMBER: US/10/178,449A  
 PRIOR FILING DATE: 2000-05-03  
 PRIOR APPLICATION NUMBER: US 10/030,516  
 PRIOR FILING DATE: 2000-05-03  
 PRIOR APPLICATION NUMBER: PCT/US00/11952  
 PRIOR FILING DATE: 2000-05-03  
 PRIOR APPLICATION NUMBER: US 60/133,039  
 PRIOR FILING DATE: 1999-05-07  
 NUMBER OF SEQ ID NOS: 51  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO: 9  
 LENGTH: 463

Query Match Score 35.1%; Best Local Similarity 77.2%; Matches 190; Conservative 0; Pred. No. 2.7e-33; Gaps 0;  
 ORGANISM: Parthenium argentatum Grey  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: 413 \_ OTHER INFORMATION: n = A, T, C or G  
 us-10-178-449A-9

Db 154 TTGTTGTAACACAGACTTGACGACAACTTATGGAGGGTGCGCCATGG 274  
 Db 94 AGAAATCGATCGGTGAAACGGGAGACATGTGAGGAACTGTGTTGAA 214  
 Qy 215 CTGTGGCAATAACGGGACATGTGACAACCAATTAAATCATGGAGGGTGCGCCATGG 274  
 Db 154 TTGTTGTAACACAGACTTGACGACAACTTATGGAGGGTGCGCCATGG 213  
 Qy 275 AGCGTGTATGTGGTAACGGGAAACAGATGTGTTCTTACTCAATTGTAAGGC 334  
 Db 214 AGCTGTATGTGGGTGGAAACACATGTGCTTCCTACTTCCAGTGC 273  
 Qy 335 CGAAAAGCTGTGTCAGAACAAACTTAAAGCGAAACACTTAATGC 394

Db 274 CGAGAAGATGCCAGGATAACTCGAGCTGAAGAGCTTCCAAAGGAAGATGAAAGC 333  
 Qy 395 CCAAA 400  
 Db 334 TGAAA 339

**RESULT 8**  
 US-10-178-449A-11  
 Sequence 11, Application US/10178449A  
 Publication No. US20030140368A1  
 GENERAL INFORMATION  
 APPLICANT: Famodu, Omolayo O.  
 APPLICANT: Herrmann, Rafael L.  
 APPLICANT: Lu, Albert L.  
 APPLICANT: McCutchen, Billy Fred  
 APPLICANT: Miao, Guo-Hua  
 APPLICANT: Presnail, James K.  
 APPLICANT: Rafalski, Jan Antoni  
 APPLICANT: Weng, Zude  
 TITLE OF INVENTION: Plant Defensins  
 FILE REFERENCE: 35718/249123  
 CURRENT FILING DATE: 2002-06-21  
 PRIOR APPLICATION NUMBER: US 10/030,516  
 PRIOR FILING DATE: 2000-05-03  
 PRIOR APPLICATION NUMBER: PCT/US00/11952  
 PRIOR FILING DATE: 2000-05-03  
 PRIOR APPLICATION NUMBER: US 60/133,039  
 PRIOR FILING DATE: 1999-05-07  
 NUMBER OF SEQ ID NOS: 51  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO: 11  
 LENGTH: 603

Query Match Score 35.1%; Best Local Similarity 77.2%; Matches 190; Conservative 0; Pred. No. 3e-33; Gaps 0;  
 ORGANISM: Parthenium argentatum Grey  
 us-10-178-449A-11

Qy 155 AGATATCGCATCGCTTAGTGAGAACATGTGAGAAAGCTAGGAA 214  
 Db 101 AGAAATCGATCGTAGGGAGAACATGTGAGAAAGCTAGGAA 160  
 Qy 215 CTGTGGCAATAACGGGACATGTGACAACCAATTAAATCATGGAGGGTGCGCCATGG 274  
 Db 161 TTGTTGTAACACAGACATGTGAGGAACTCAAGTCTGGAGGGTGCAGCCATGG 220  
 Qy 275 AGCGTGTATGTGGTAACGGGAAACACATGTGTTACTTCAATTGTAAGGC 334  
 Db 221 AGCTTGTATGTGGGGGGAAACACATGTGCTCTGCTACTCCAGTGCAGCTGAA 280  
 Qy 335 CGAAAAGCTGTGTCAGAACAAACTTAAAGCGAAACACTTAATGC 394  
 Db 281 CGAGAAGATGCCAGGATAACCTCGAGCTGAAGAGTTGCCAAAGGC 340

RESULT 9  
 US-10-178-449A-21  
 Sequence 21, Application US/10178449A  
 Publication No. US20030140368A1  
 GENERAL INFORMATION  
 APPLICANT: Famodu, Omolayo O.  
 APPLICANT: Herrmann, Rafael L.  
 APPLICANT: McCutchen, Billy Fred  
 APPLICANT: Miao, Guo-Hua



Qy 215 CTGGGAAATACGGGACATTGTGACACACCAATGTAATACTGGAGGGTGGGCCATGG 274  
 Db 159 ATGGGAAAGAAAAACACTGTGATGACCATGTCATGGGGGGCAGGG 218  
 Qy 275 ACGGTGTCATGTGCGTAACGGGAAACACATGTGATGACCATGTCATGGGGGGCAGGG 234  
 Db 219 AGCTTGTCACGTGCGATGGAAACACATGTGTCATGTCATGGCCAGGC 278  
 Qy 335 CGAAAAGCTTGTCAAGAACAAACTTAAAGCGGAACACTGGCTCAAGAACAAACTTAATGC 394  
 Db 279 CCAGAAGTGGCTACGATAAACCTCAGAGCGAAAGGTGGCTGCCAAGGAAAGATGAAACC 338  
 Qy 395 CCAAAG 401  
 Db 339 CGAAAG 345

---

RESULT 12  
 US-10-636-026-6  
 ; Sequence 6, Application US/10636026  
 ; Publication No. US2004011171A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bidney, Dennis L.  
 ; APPLICANT: Crasta, Oswald R.  
 ; APPLICANT: Duvick, Jon  
 ; APPLICANT: Hu, Guihua  
 ; TITLE OF INVENTION: Sunflower Anti-Pathogenic Proteins and  
 ; TITLE OF INVENTION: Genes and their Uses  
 ; FILE REFERENCE: 571-8-90  
 ; CURRENT APPLICATION NUMBER: US/10/636,026  
 ; CURRENT FILING DATE: 2003-08-07  
 ; PRIOR APPLICATION NUMBER: US/09/589,733C  
 ; PRIOR FILING DATE: 2000-06-08  
 ; PRIOR APPLICATION NUMBER: 6/0/140,646  
 ; PRIOR FILING DATE: 1999-06-23  
 ; PRIOR APPLICATION NUMBER: 6/0/162,904  
 ; PRIOR FILING DATE: 1999-11-01  
 ; NUMBER OF SEQ ID NOS: 41  
 ; LENGTH: 565  
 ; SOFTWARE: FastSEQ for Windows Version 3.0  
 ; SEQ ID NO 6  
 ; TYPE: DNA  
 ; ORGANISM: Helianthus annuus  
 US-10-636-026-6

Query Match 34.6%; Score 154.2; DB 18; Length 565;  
 Best Local Similarity 76.5%; Pred. No. 1.2e-32;  
 Matches 189; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

Qy 155 AGATATGCAATACGGGACATTGTGACACACCATGTAATCTGGGGGTGGCCATGG 274  
 Db 99 AGAAATGGATGGTGGTGAAGGAGAACATGTGAGGGAGAACATGTGAGGGATGGAA 153

Qy 215 CTGTCGCAATACGGGACATTGTGACACACCATGTAATCTGGGGGTGGCCATGG 274  
 Db 154 TTGGTTAACAAACACATGTGAGGACCATGTAATCTGGGGGTGGCCATGG 213

Qy 275 AGCGTGTCAATGTGCAACGGAAACACATGTGTTTCTGTACTTCATGTAAAGC 334  
 Db 214 AGCTTGTCACTGTGCGGTGGAAACACATGTGCTCTGTACTTCATGTAAAGC 273

Qy 335 CGAAAGCTGTCATGCAACACTTAAGCGGAACACTGGCTCAAGAACACTTAATGC 394  
 Db 274 CGAGAGATGCCCTGGATAAACTCGAGAGCTGGCTGCCAAGGAGAGATGAACT 333

Qy 395 CCAAAG 400  
 Db 334 TGAAA 339

---

RESULT 14  
 US-10-17-449A-23  
 ; Sequence 23, Application US/10178449A  
 ; Publication No. US20030140368A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Famodu, Omolayo O.  
 ; APPLICANT: Hermann, Rafael  
 ; APPLICANT: Lu, Albert L.  
 ; APPLICANT: McCutchen, Billy Fred  
 ; APPLICANT: Miao, Guo-Hua  
 ; APPLICANT: Prehnall, James K.  
 ; APPLICANT: Rafalski, Jan Antoni  
 ; APPLICANT: Weng, Zude  
 ; TITLE OF INVENTION: Plant Defensins

Qy 275 AGCGTGTCAATGTGCAACGGAAACACATGTGTTTCTGTACTTCATGTAAAGC 334  
 Db 219 AGCTTGTCACTGTGCGGTGGAAACACATGTGCTCTGTACTTCATGTAAAGC 278

Qy 335 CGAAAGCTGTCATGCAACACTTAAGCGGAACACTGGCTCAAGAACACTTAATGC 394  
 Db 279 CCAGAAGTGGCTACGATAAACCTCAGAGCGAAAGGTGGCTGCCAAGGAGAGATGAACT 338

Qy 395 CCAAAG 401  
 Db 339 CGAAAG 345

FILE REFERENCE: 35718/249123  
 CURRENT APPLICATION NUMBER: US/10/178,449A  
 CURRENT FILING DATE: 2002-06-21  
 PRIORITY NUMBER: US/10/030,516  
 PRIORITY NUMBER: 2000-05-03  
 PRIORITY NUMBER: PCT/US00/11952  
 PRIORITY NUMBER: 2000-05-03  
 PRIORITY NUMBER: US 60/133,039  
 PRIORITY NUMBER: 1999-05-07  
 NUMBER OF SEQ ID NOS: 51  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO: 23

TYPE: DNA  
 ORGANISM: Parthenium argentatum Grey  
 FEATURE: misc\_feature  
 NAME/KEY: misc\_feature  
 LOCATION: 368  
 OTHER INFORMATION: n = A, T, C or G  
 US-10-178-449A-23

Query Match 34.3%; Score 153.2%; DB 15; Length 472;  
 Best Local Similarity 76.4%; Pred. No. 2.1e-32;  
 Matches 188; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

Qy 15 AGATATGCAATCGTTAGTGGAGAACTATGGAGAAAGCTAGCAAGAACATGTGGAA 214  
 Db 86 AGAAATCGATCGTCGTTAGGGAGAACTTGACAAACACTGGCCATGG 274  
 Qy 215 CTGTGCCAATACGGGACATTTGGACAAACCAATGTAATCATGGAGG 274  
 Db 146 TTGTGTCATAACAGAACATGGACCAATGCAAGTGGAGG 205

Query Match 34.3%; Score 153.2%; DB 15; Length 472;  
 Best Local Similarity 76.4%; Pred. No. 2.1e-32;  
 Matches 188; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

Qy 155 AGATATGCATCGTTAGTGGAGAACTATGGAGAAAGCTAGCAAGAACATGTGGAA 214  
 Db 93 AGAAATCGATCGTCGTTAGGGAGAACTATGGAGGCAAGAACATGTGGAA 152

Query Match 31.0%; Score 138.4%; DB 15; Length 439;  
 Best Local Similarity 71.9%; Pred. No. 2.8e-28;  
 Matches 192; Conservative 0; Mismatches 74; Indels 1; Gaps 1;

Qy 215 CTGTGCCAATACGGGACATTTGGAGGGTAGCAAGAACATGTGGCCATGG 274  
 Db 153 TTGTGTCATAACAGAACATGGACCAATGCAAGTGGAGG 212

Query Match 31.0%; Score 138.4%; DB 15; Length 439;  
 Best Local Similarity 71.9%; Pred. No. 2.8e-28;  
 Matches 192; Conservative 0; Mismatches 74; Indels 1; Gaps 1;

Qy 275 AGCGTGTCAATGCTTAACGGGAAACACATGTGTACTCTAATTGTAAAAAGC 334  
 Db 213 AGCTTGTCAATGCGCGTGGAAACATGTGGCTACTTCAGTGCCTCAAAGC 272

Query Match 33.5%; Score 138.4%; DB 15; Length 439;  
 Best Local Similarity 71.9%; Pred. No. 2.8e-28;  
 Matches 192; Conservative 0; Mismatches 74; Indels 1; Gaps 1;

Qy 335 CGAAAGCTTCCTCAA-GACAACCTAAAGCGAAACAACCTGGCTCAAGACAACCTTAATG 393  
 Db 273 CGAAAGATGCCANGGATAAACCTCGAGTGTGAAGAAGCTTGCAAGGAAGATGAA 332

Query Match 39.4%; Score 153.2%; DB 15; Length 472;  
 Best Local Similarity 76.4%; Pred. No. 2.1e-32;  
 Matches 188; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

Qy 394 CCCAAAGCTTGACCGTGATGCCAAGA 420  
 Db 333 GCTGAAAAGGCCAGNCAACCTGA 359

Search completed: March 18, 2005, 19:33:33  
 Job time : 422 secs

RESULT 15  
 US-10-178-449A-15  
 Sequence 15, Application US/10178449A  
 Publication No. US20030140368A1  
 GENERAL INFORMATION:  
 APPLICANT: Pamodu, Omolayo O.  
 APPLICANT: Herrmann, Rafael  
 APPLICANT: Lu, Albert L.  
 APPLICANT: McCutchen, Billy Fred  
 APPLICANT: Miao, Guo-Hua  
 APPLICANT: Presnail, James K.  
 APPLICANT: Rafalski, Jan Antoni  
 APPLICANT: Weng, Zude  
 TITLE OF INVENTION: Plant Defensins  
 FILE REFERENCE: 35718/249123  
 CURRENT APPLICATION NUMBER: US/10/178,449A  
 CURRENT FILING DATE: 2002-06-21  
 PRIORITY NUMBER: US 60/10/030,516  
 PRIORITY NUMBER: 2000-05-03  
 PRIORITY NUMBER: PCT/US00/11952  
 PRIORITY NUMBER: 2000-05-03  
 PRIORITY NUMBER: US 60/133,039  
 PRIORITY NUMBER: 1999-05-07  
 NUMBER OF SEQ ID NOS: 51  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO: 15  
 LENGTH: 439

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Copyright (c) 1993 - 2005 Compugen Ltd.		BQ988151	QGF14C09.
OM nucleic	nucleic search, using sw model	BQ012833	QGJ3A06.Y
Run on:	March 18, 2005, 12:39:02 ; Search time 7103 Seconds (without alignments)	CN253987	B1D0051.B
Title:	US-09-763-019-5	BU014798	QGJ8G14.Y
Perfect score:	446	BU012812	QGJ2P08.Y
Sequence:	1 atgtgaaatcggttgtgc.....ttccaaacgttgaacatccg 446	BU0981882	QGF14P10.
Scoring table:	IDENTITY_NUC	C0553309	SA_MP_01.
Gapop 10.0 , Gapext 1.0	2390.070 Million cell updates/sec	C0553533	SA_MP_01.
Searched:	34239544 seqs, 19032134700 residues	CO55393	BU009853.QGJ1W09.
Total number of hits satisfying chosen parameters:	68479088	BU009853	BU009853.QGJ1W09.
Minimum DB seq length:	0	BU012626	BU012626.QGJ2H01.Y
Maximum DB seq length:	2000000000	BU011459	QGU16E18.
Post-processing: Minimum Match 0%		AV786126	AV786126.
Maximum Match 100%		AV824429	AV824429.
Listing first 45 summaries		CN847468	PG0704370
Database :	EST:*	BH657225	BOCGJA18TP
	1: gb_est1:*	CL504812	CL504812.
	2: gb_est2:*	SAIL743	SAIL743.
	3: gb_htc:*	CL504811	CL504811, mRNA sequence.
	4: gb_est3:*	AV786126	AV786126.
	5: gb_est4:*	AV824429	AV824429.
	6: gb_est5:*	C0749420	C0749420.KBFAE001.P
	7: gb_est6:*	BH473290	BH473290.BOGXA16TP
	8: gb_gss1:*	CF270036	CF270036.2H4_Caps1
	9: gb_gss2:*	BG321454	BG321454.D801_08N0
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.		ALIGNMENTS	
SUMMARIES		RESULT 1	
Result No.	Score	Query Match Length DB ID	Description
1	198.6	44.5	BQ989575 QGF18A17
2	197	44.2	BQ984300 QGE21E24.
3	197	44.2	BQ984745 QGB4h04.Y
4	197	44.2	BU008575 QGH7P24.Y
5	177.2	39.7	BQ995419 QCF9P04.Y
6	160.6	36.0	AJ412176 AJ412176
7	154.2	34.6	CD846862 DH0AB51ZB
8	153.6	34.4	AJ541276 AJ541276
9	131.2	29.4	BQ844100 QGA12M13.
10	127	28.5	AJ541406 AJ541406
11	127	28.5	AJ541283 AJ541283
12	123.6	27.7	BQ847005 QGA20020.
13	122	27.4	AU306450 AU306450
14	100.2	22.5	AJ541276 AJ541276
15	94	21.1	BQ945488 QGA16N20.
16	94	21.1	BQ961273 QGC18A12.
17	77.6	17.4	BU011479 QGJ16F16.
18	76	17.0	BU014657 QGJ7P01.Y
19	76	17.0	BU011346 QGJ15P15.
20	76	17.0	BQ990734 QGP20P11.
21	76	17.0	BU012409 QGJ11N15.Y
22	76	17.0	BU014714 QGJ8C12.Y
23	76	17.0	BU014714 QGJ8C12.Y
24	76	17.0	BQ990122 QSF19114.
FEATURES		Source	
COMMENT		Location/Qualifiers	
AUTHORS		Contact: Alexander Kozik [R.W.Michelmore] Department of Vegetable Crops, R.W.Michelmore Lab University of California at Davis (UCD) Alderson Hall, UCD, Davis, CA 95616, USA Tel: 1-(530)-742-1742 Ellison, P., van Damme, M., Lavelle, D., Chevalier, P., Ziegie, J., Lai, Z., Church, S., Livingston, K., Zhou, Y., Bradford, K. Email: akozik@atgc.org [michelmore@ucdavis.edu] belongs to contig QG_CA_Contig6866, see http://cgpdb.ucdavis.edu/ for details.	
REFERENCE		http://compgenomics.ucdavis.edu/ Unpublished (2002)	
TITLE		Lettuce and Sunflower ESTs from the Composite Genome Project	
JOURNAL		http://compgenomics.ucdavis.edu/	
COMMENT		1 (bases 1 to 604)	
AUTHORS		Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L., Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegie,J., Ellison,P., Kollman,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z., Church,S., Jackson,L. and Bradford,K.	
REFERENCE		1 (bases 1 to 604)	
TITLE		Lettuce and Sunflower ESTs from the Composite Genome Project	
JOURNAL		http://compgenomics.ucdavis.edu/	
COMMENT		1 (bases 1 to 604)	
AUTHORS		Contact: Alexander Kozik [R.W.Michelmore] Department of Vegetable Crops, R.W.Michelmore Lab University of California at Davis (UCD) Alderson Hall, UCD, Davis, CA 95616, USA Tel: 1-(530)-742-1742 Ellison, P., van Damme, M., Lavelle, D., Chevalier, P., Ziegie, J., Lai, Z., Church, S., Livingston, K., Zhou, Y., Bradford, K. Email: akozik@atgc.org [michelmore@ucdavis.edu] belongs to contig QG_CA_Contig6866, see http://cgpdb.ucdavis.edu/ for details.	
REFERENCE		http://compgenomics.ucdavis.edu/	
TITLE		Lettuce and Sunflower ESTs from the Composite Genome Project	
JOURNAL		http://compgenomics.ucdavis.edu/	
COMMENT		1 (bases 1 to 604)	
AUTHORS		Contact: Alexander Kozik [R.W.Michelmore] Department of Vegetable Crops, R.W.Michelmore Lab University of California at Davis (UCD) Alderson Hall, UCD, Davis, CA 95616, USA Tel: 1-(530)-742-1742 Ellison, P., van Damme,M., Lavelle,D., Chevalier,P., Ziegie,J., Lai,Z., Church,S., Livingston,K., Zhou,Y., Lai,Z., Jackson,L. and Bradford,K.	
REFERENCE		1 (bases 1 to 604)	
TITLE		Lettuce and Sunflower ESTs from the Composite Genome Project	
JOURNAL		http://compgenomics.ucdavis.edu/	
COMMENT		1 (bases 1 to 604)	
AUTHORS		Contact: Alexander Kozik [R.W.Michelmore] Department of Vegetable Crops, R.W.Michelmore Lab University of California at Davis (UCD) Alderson Hall, UCD, Davis, CA 95616, USA Tel: 1-(530)-742-1742 Ellison, P., van Damme,M., Lavelle,D., Chevalier,P., Ziegie,J., Lai,Z., Church,S., Livingston,K., Zhou,Y., Lai,Z., Jackson,L. and Bradford,K.	
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TITLE		Lettuce and Sunflower ESTs from the Composite Genome Project	
JOURNAL		http://compgenomics.ucdavis.edu/	
COMMENT		1 (bases 1 to 604)	
AUTHORS		Contact: Alexander Kozik [R.W.Michelmore] Department of Vegetable Crops, R.W.Michelmore Lab University of California at Davis (UCD) Alderson Hall, UCD, Davis, CA 95616, USA Tel: 1-(530)-742-1742 Ellison, P., van Damme,M., Lavelle,D., Chevalier,P., Ziegie,J., Lai,Z., Church,S., Livingston,K., Zhou,Y., Lai,Z., Jackson,L. and Bradford,K.	
REFERENCE		1 (bases 1 to 604)	
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JOURNAL		http://compgenomics.ucdavis.edu/	
COMMENT		1 (bases 1 to 604)	
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TITLE		Lettuce and Sunflower ESTs from the Composite Genome Project	
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REFERENCE		1 (bases 1 to 604)	
TITLE		Lettuce and Sunflower ESTs from the Composite Genome Project	
JOURNAL		http://compgenomics.ucdavis.edu/	
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AUTHORS		Contact: Alexander Kozik [R.W.Michelmore] Department of Vegetable Crops, R.W.Michelmore Lab University of California at Davis (UCD) Alderson Hall, UCD, Davis, CA 95616, USA Tel: 1-(530)-742-1742 Ellison, P., van Damme,M., Lavelle,D., Chevalier,P., Ziegie,J., Lai,Z., Church,S., Livingston,K., Zhou,Y., Lai,Z., Jackson,L. and Bradford,K.	
REFERENCE		1 (bases 1 to 604)	
TITLE		Lettuce and Sunflower ESTs from the Composite Genome Project	
JOURNAL		http://compgenomics.ucdavis.edu/	
COMMENT		1 (bases 1 to 604)	
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REFERENCE		1 (bases 1 to 604)	
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JOURNAL		http://compgenomics.ucdavis.edu/	
COMMENT		1 (bases 1 to 604)	
AUTHORS		Contact: Alexander Kozik [R.W.Michelmore] Department of Vegetable Crops, R.W.Michelmore Lab University of California at Davis (UCD) Alderson Hall, UCD, Davis, CA 95616, USA Tel: 1-(530)-742-1742 Ellison, P., van Damme,M., Lavelle,D., Chevalier,P., Ziegie,J., Lai,Z., Church,S., Livingston,K., Zhou,Y., Lai,Z., Jackson,L. and Bradford,K.	
REFERENCE		1 (bases 1 to 604)	
TITLE		Lettuce and Sunflower ESTs from the Composite Genome Project	
JOURNAL		http://compgenomics.ucdavis.edu/	
COMMENT		1 (bases 1 to 604)	
AUTHORS		Contact: Alexander Kozik [R.W.Michelmore] Department of Vegetable Crops, R.W.Michelmore Lab University of California at Davis (UCD) Alderson Hall, UCD, Davis, CA 95616, USA Tel: 1-(530)-742-1742 Ellison, P., van Damme,M., Lavelle,D., Chevalier,P., Ziegie,J., Lai,Z., Church,S., Livingston,K., Zhou,Y., Lai,Z., Jackson,L. and Bradford,K.	
REFERENCE		1 (bases 1 to 604)	
TITLE		Lettuce and Sunflower ESTs from the Composite Genome Project	
JOURNAL		http://compgenomics.ucdavis.edu/	
COMMENT		1 (bases 1 to 604)	
AUTHORS		Contact: Alexander Kozik [R.W.Michelmore] Department of Vegetable Crops, R.W.Michelmore Lab University of California at Davis (UCD) Alderson Hall, UCD, Davis, CA 95616, USA Tel: 1-(530)-742-1742 Ellison, P., van Damme,M., Lavelle,D., Chevalier,P., Ziegie,J., Lai,Z., Church,S., Livingston,K., Zhou,Y., Lai,Z., Jackson,L. and Bradford,K.	
REFERENCE		1 (bases 1 to 604)	
TITLE		Lettuce and Sunflower ESTs from the Composite Genome Project	
JOURNAL		http://compgenomics.ucdavis.edu/	
COMMENT		1 (bases 1 to 604)	
AUTHORS		Contact: Alexander Kozik [R.W.Michelmore] Department of Vegetable Crops, R.W.Michelmore Lab University of California at Davis (UCD) Alderson Hall, UCD, Davis, CA 95616, USA Tel: 1-(530)-742-1742 Ellison, P., van Damme,M., Lavelle,D., Chevalier,P., Ziegie,J., Lai,Z., Church,S., Livingston,K., Zhou,Y., Lai,Z., Jackson,L. and Bradford,K.	
REFERENCE		1 (bases 1 to 604)	
TITLE		Lettuce and Sunflower ESTs from the Composite Genome Project	
JOURNAL		http://compgenomics.ucdavis.edu/	
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AUTHORS		Contact: Alexander Kozik [R.W.Michelmore] Department of Vegetable Crops, R.W.Michelmore Lab University of California at Davis (UCD) Alderson Hall, UCD, Davis, CA 95616, USA Tel: 1-(530)-742-1742 Ellison, P., van Damme,M., Lavelle,D., Chevalier,P., Ziegie,J., Lai,Z., Church,S., Livingston,K., Zhou,Y., Lai,Z., Jackson,L. and Bradford,K.	
REFERENCE		1 (bases 1 to 604)	
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REFERENCE		1 (bases 1 to 604)	
TITLE		Lettuce and Sunflower ESTs from the Composite Genome Project	
JOURNAL		http://compgenomics.ucdavis.edu/	



source	1. . 620 /organism="Lactuca sativa" /mol_type="mRNA" /cultivar="L. serriola" /clone="QCB4h04" /db_xref="taxon:4236" /lab_host="E.coli" /note="Vector: pBRCDNAStAB; The library was constructed from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://cgpdb.ucdavis.edu/ TAG TISSUE=germinating seeds TAG_LIB=QG_EFGHJ lettuce serriola TAG_SEQ=TCTGTGCGGG"	
ORIGIN		
Query Match	44.2%; Score 197; DB 5; Length 620; Best Local Similarity 81.7%; Pred. No. 2e-42; Matches 241; Conservative 0; Mismatches 50; Indels 4; Gaps 1;	
Qy	155 AGATATGCCATCGTGTAGTTGAGAAACTATGGCAGAAAGCTGGCAAGACATGGTCGGAAA 214 Db 106 AGATATGCCAGACTGTGAGGGAAACTATGGCAGAAACCTACCAAGACATGGTCGGAAA 165 Qy 215 CTGTGGCATATACGGACATTGGACACAACTGAATCATGGAGGGTGGGCCATGG 274 Db 166 CTGTGGCAACACGGACACTGGCATGCGCACATCTGGAGGGTGGAGCCATGG 225 Qy 275 ACGGTGTGATGTGCGTAACGGGAAACCATGGACATTGTGAAAAAGC 334 Db 226 ACCATGGTACGTGCGTGAGGGAAACCATGTGCTCTGGTACTTAAATGTCTTAAGC 285 Qy 335 CGAAAAGCTTGTGCTCAAGAACACTTAAAGGCCAACACTCGCTCAAGAACCTTAATGC 394 Db 286 TAAAAGCTTGTGCCAACGAAACTCAAGCCAAGGCTCGCCCAAGAACCTCAAGC 345 Qy 395 CGAAAAGCTTGTGCTCAAGAACACTTAAAGGCCAACACTCGCTCAAGAACACTTAATGC 445 Db 346 TAAAAGCTTGTGCCAACGAAACTCAAGCCAAGGCTCGCCCAAGAACCTCAAGC 400 Db 307 TGAAAGCTTGTGCCAACGAAACTCAAGCCAAGGCTCGCCCAAGAACACTCAAGC 366 Qy 395 CGAAAAGCTTGTGCTG --- -TGATGCCAGAAGTGTGTTCAACACGTTGAACTCC 445 Db 367 TAAAAGCTTGTGCCAACGAAAGTGTGACCTAAATGTGACCATCC 421	
RESULT 4		
LOCUS	BU008575	641 bp mRNA linear EST 22-AUG-2002
DEFINITION	QGH_P24.yg_ab1	QG_EFGHJ lettuce serriola cDNA clone
ACCESSION	BU008575	
VERSION	BU008575.1	GT:22442970
KEYWORDS		
SOURCE	Lactuca sativa	
ORGANISM	Bukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eu dicotyledons; core eudicots; asterids; campanulids; Asterales; Asteraceae; Cichorioideae; Cichorieae; Lactuceae; Lactuca sativa	
REFERENCE	Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L., Lin,H., van Damme,M., Lavelle,D., Ziegler,J., Ellison,P., Kolkman,J., Slabbaugh,M.S., Livingston,K., Zhou,Y., Lai,Z., Church,S., Jackson,L. and Bradford,K.	
AUTHORS	Unpublished (2002)	
JOURNAL	Contact: Alexander Kozik [R.W.Michelmore] Department of Vegetable Crops, R.W.Michelmore Lab University of California at Davis (UCD) Asmundson Hall, UCD, Davis, CA 95616, USA	
COMMENT	http://compgenomics.ucdavis.edu/ http://compositae.genome Project Lettuce and Sunflower ESTs from the Compositae Genome Project http://compgenomics.ucdavis.edu/	

Tel: 1-(530)-742-1742  
Fax: 1-(530)-752-1659  
Email: akozik@atgc.org [michelmore@veggmail.ucdavis.edu]  
belongs to contig QG\_CA\_Contig6866, see <http://cgpdb.ucdavis.edu/>  
for details.  
Plate: QGH7 row: P column: 24.  
Location/Qualifiers  
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/db\_xref="taxon:4236"  
/clone="QGH7P4"  
/lab\_host="E.coli"  
/clone\_lib="QG\_EFGHJ lettuce serriola"  
/note="Vector: pBRCDNAStAB; The library was constructed from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://cgpdb.ucdavis.edu/  
TAG TISSUE=germinating seeds  
TAG\_LIB=QG\_EFGHJ lettuce serriola  
TAG\_SEQ=Not found"

FEATURES SOURCE

Query Match Score 197; DB 5; Length 641;  
Best Local Similarity 81.7%; Pred. No. 2e-42;  
Matches 241; Conservative 0; Mismatches 50; Indels 4; Gaps 1;

Qy 155 AGATATGCCATCGTGTAGTTGAGAACTATGGCAGAAAGCTGGCAAGACATGGTCGGAAA 214  
Db 127 AGATATGCCATCGTGTAGTTGAGAACTATGGCAGAAAGCTGGCAAGACATGGTCGGATAA 186  
Qy 155 AGATATGCCATCGTGTAGTTGAGAACTATGGCAGAAAGCTGGCAAGACATGGTCGGAAA 214  
Db 187 CTGTGGCAACACGGACACTGTGATGCCACTGTGCTGAGGACTCTGGCAATCTGGCTGAGCCATGG 246  
Qy 215 CTGTGGCAATACGGACATTTGTGACACAACTGTGAAATCATGGAGGGTGGGCCATGG 274  
Db 275 AGGTGTGATGTGCTTAACGGAAACATGGACATTGTGAAATCATGGAGGGTGGGCCATGG 334  
Qy 275 AGGTGTGATGTGCTTAACGGAAACATGGACATTGTGAAATCATGGAGGGTGGGCCATGG 334  
Db 247 AGCATGTCACGTGCGTGAGGGAAACATGTGCTCTGGTACTTAAATGTCTTAAGC 306  
Qy 335 CGAAAAGCTTGTGCTCAAGAACACTTAAAGGCCAACACTCGCTCAAGAACACTTAATGC 394  
Db 307 TGAAAGCTTGTGCCAACGAAACTCAAGCCAAGGCTCGCCCAAGAACCTCAAGC 366  
Qy 395 CGAAAAGCTTGTGCTG --- -TGATGCCAGAAGTGTGTTCAACACGTTGAACTCC 445  
Db 367 TAAAAGCTTGTGCCAACGAAAGTGTGACCTAAATGTGACCATCC 421

RESULT 5

LOCUS BQ95419

DEFINITION OGSP04.yg\_ab1 OG\_EFGHJ lettuce serriola cDNA clone

VERSION BQ95419.1 GI:22414954

KEYWORDS EST.

SOURCE Lactuca sativa

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eu dicotyledons; core eudicots; asterids; campanulids; Asterales; Asteraceae; Cichorioideae; Cichorieae; Lactuceae; Lactuca sativa

REFERENCE 1 (bases 1 to 641)

AUTHORS Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegler,J., Ellison,P., Kolkman,J., Slabbaugh,M.S., Livingston,K., Zhou,Y., Lai,Z., Church,S., Jackson,L. and Bradford,K.

JOURNAL Unpublished (2002)

COMMENT Contact: Alexander Kozik [R.W.Michelmore]  
Department of Vegetable Crops, R.W.Michelmore Lab  
University of California at Davis (UCD)  
Asmundson Hall, UCD, Davis, CA 95616, USA



FEATURES	source	Location/Qualifiers
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/clone.Lib="Hdavr1"		
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Pred. No.	8e-31;	
0; Mismatches	58;	Indels 0;
Gaps 0;		
Qy	155	AGATATCGGATTCGGTATGGAACTATGCCAGAACATGGCAAGCTTAATGCAAGACATGGCAATGGAA 214
Db	97	AGAAATCGGATTCGGTGAAGGGAATTATGTGAGAAGGGAAC 156
Qy	215	CCTGGGATACTGGGACATTGTGACACAATGTAATCATGGGGGGCCATGG 274
Db	157	ATGGGAGAACACTGTGCAACTCTGGAGCCATGG 216
RESULT 9		
Qy	275	ACGGTGATCGCTGAAACACATGTTCTGTACTCTAAATGTAAGGC 334
Db	217	AGCTTGACGCTGCGGTGGAAACACATGTCCTCTGTACTCTAAAGC 276
Qy	335	CGAAAAGCTGTCAAGCAAACTTAAGGCCAACACTTAATGTC 394
Db	277	CCAGAAGTGGCTCAGGTTAAACTCTCGAGCAAGGAGATGAAAC 336
Qy	395	CCAAAG 401
Db	337	CGAAAAG 343
RESULT 8		
AJ541276		475 bp mRNA linear EST 04-MAY-2004
LOCUS		AJ541276 HdpBRI Helianthus annuus cDNA clone H00003R05, mRNA
DEFINITION		sequence.
ACCESSION		AJ541276
KEYWORDS		EST.
SOURCE		Helianthus annuus (common sunflower)
ORGANISM		Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicots; asterids; campanulids; Asterales; Asteridae; Heliantheae; Helianthus.
REFERENCE		1 (bases 1 to 475) Aubrionguy,C., Ben,C., Liboz,T. and Gentzbittel,L. Sequence evaluation of four specific cDNA libraries for developmental genomics of sunflower.
AUTHORS		Contact: Tamborindeuy C.
TITLE		Laboratoire de Biotechnologie et Amélioration des Plantes Institut National Polytechnique de Toulouse Supérieure Agronomie de Toulouse IFR40, Pole de Biotechnologie Vegetale, 18 chemin de Borde Rouge, Auzette, CASTANET TOLOSAN 31326, France.
JOURNAL		1. . . . .
COMMENT		Location/Qualifiers
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1.	.475	/organism="Helianthus annuus" /mol_type="mRNA" /cultivar="Emi1" /db_xref="txon:4232" /clone="H00003R05" /tissue_type="hypocotyl" /cell_type="protoplasm" /dev_stage="1- to 5-days old protoplast" /clone.Lib="HdpBRI"
ORIGIN		

Query Match 34.4%; Score 153.6; DB 1; Length 475;  
 Best Local Similarity 77.5%; Pred. No. 1.1e-30;  
 Matches 186; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

Qy 162 GCATCCGTTAGTGGAGAACATGGCAAGACATGGCTGGAAACTGGACATGGCTGGGG 221  
 Db 4 GGATCCGTTAGGAAAGGAAATTATGCGAAGGCAAGGCAAGATGGCTGGAAAATGTCGC 63

Qy 222 AATACGGACATTTGATGCAACATGAACTTCAATTGTAAGGCGAAAG 281  
 Db 64 AACACAGAACACTGTGATGACAGTCAGCTGGAGGGTGGCCATGGCTGT 123

Qy 282 CATGTGGTAAAGGGAAACACATGTTCTGTACTTCATTGTAAGGCGAAAG 341  
 Db 124 CTATGGCGGTGGAAACACTGTGCTTCAGTCTCAAGGCCAGAG 183

Qy 342 CTGGCTCAAGACAACAACTTAAGGCCAACAACTGCTCAAGGAA 401  
 Db 184 TTGGCTCAGGATAAACTCAGGCCAGAGACTGCGGAGATTGAAAGG 243

RESULT 9

Q0844100 BQ844100 239 bp mRNA linear EST 14-AUG-2002

LOCUS QGA12M13.yg\_ab1 OG ABCD1 lettuce salinas Lactuca sativa cDNA clone QGA12M13, mRNA sequence.

DEFINITION Q0844100

ACCESSION BQ844100.1 GI:22224503

VERSION EST.

KEYWORDS SOURCE Lactuca sativa

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicots; core eudicots; asterids; campanulids; Asterales; Asteridae; Cichorioideae; Cichorioeae; Lactuca.

1 (bases 1 to 239)

REFERENCE AUTHORS Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L., Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegler,J., Ellison,P., Kolkman,J., Slaoui,M., Livingston,K., Zhou,Y., Lai,Z., Church,S., Jackson,I. and Bradford,K.

TITLE Lettuce and Sunflower ESTs from the Compositae Genome Project

JOURNAL COMMENT Unpublished (2002)

CONTACT Alexander Kozik [R.W.Michelmore]  
Department of Vegetable Crops, R.W.Michelmore Lab  
University of California at Davis  
Asmundson Hall, UCD, Davis, CA 95616, USA  
Tel: 1-(530)-742-1742  
Fax: 1-(530)-752-9659  
Email: akozik@atgc.org [michelmore@veggmail.ucdavis.edu]  
belongs to contig QS\_CA\_Comicg6866, see <http://egpdb.ucdavis.edu/> for details.

FEATURES source Plate: QGA12 row: M column: 13.

1. . . . . Location/Qualifiers

/organism="Lactuca sativa"  
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/note="Vector: pBRCDNAStAB; The library was constructed from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-reactionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at <http://cgpdub.ucdavis.edu/> TAG\_SEQ=Not found"

ORIGIN	Query Match	Score 29.4%;	DB 5;	Length 239;		Qy	325 GAAAGCCAAAGCTGCTCAAGACAACTTAAGCGAACAACTCGCTCAAGACA 384
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	Matches 162;	Conservatives 0;	Mismatches 36;	Indels 1;	Gaps 1;	Qy	385 AACATTAATGCCAAAGCT 403
Oy	155 AGATATGCATCGTTAGTGAGAAGTATCGGAGAAAGTAGAGATGGTGGGAA 214					Db	184 AGATGAAAGCCGAAGGT 202
Dy	41 AAATATCACGAGTGTGAGAGAACTATSGAGAAANTAGAGAAATGGTGGGT 100						
Qy	215 CTGTGCCATTACGGGACATTGTGACAACCAATGTAATCTGGAGGGTGCGCCATGG 274					RESULT 1.1	
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Qy	275 AGCGTGTCAATGTGCTAAACGGAAACATGGTGTCTTCAATTCTGAGGGTGGGCCATGG 160					DEFINITION AJ541283_HdPsr1	Helianthus annuus cDNA clone H00003K21, mRNA sequence.
Dy	161 AGCATGTCAGTGTGGTGGGGAAACATGTGCTTCGACTTAAATTGTCCTAAAG 220					ACCESSION AJ541283	
Qy	334 CGAAAAGCTTGTCAAGA 352					VERSION AJ541283.1	GI:28370758
Dy	221 CTGAAAGCTTGGCCAA 239					KEYWORDS EST	
						ORGANISM Helianthus annuus	
							Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicots; core eudicots; asterids; campanulids; Asterales; Asteraceae; Asteroideae; Heliantheae; Helianthus.
						REFERENCE 1 (bases 1 to 420)	
						AUTHORS Tamborindeguy, C., Ben,C., Liboz,T. and Gentzbittel,L.	
						TITLE Sequence evaluation of four specific cDNA libraries for developmental genomics of sunflower	
						JOURNAL Mol. Genet. Genomics 271 (3), 367-375 (2004)	
						COMMENT Contact: Tamborindeguy C	
						Laboratoire de Biotechnologie et Amélioration des Plantes Institut National Polytechnique de Toulouse - Ecole Nationale Supérieure Agronomique de Toulouse	
						IFR40 Pole de Biotechnologie Végétale, 18 chemin de Borde Rouge, Auzet, CASTANET TOLOSAN 31326, France.	
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						Dy	4 GTTCGGAAATGTGAAACAAAGACTGTGACCACTGTGGACGTCTGGACGTG 63
						Qy	265 CGGCCATGGACGTGTCATGGCTAACGGTAACGGAAACACATGTTGTTACTTCATT 324
						Dy	64 CAGCCATGGACGTGTCATGGACTTGTGACCTGGCTGCTGTGACTTCATT 123
						Qy	325 GAAAGCCAAAGCTGCTCAAGACAACTTAAGCGAACAACTCCCTCAAGACA 384
						Dy	124 GTTCCAAAGCCAGAAGTGTGCTCAGATAACTCATAGCAAGGCTGCCAAGGAGA 183
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Oy	205 GGTGGAAACTGTGGCAATACGGGACATGTGCAACAACTGTAATGTGGAGGTG 264					Qy	385 AACATTAATGCCAAAGCT 403
Dy	4 GTTCGGAAATGTGCAACAAACATGTGACCACTGTGGACGACAGTCAGTCAGTGGGGT 63					Dy	184 AGATTGAAAGCCGAAGGT 202
Qy	265 CGGCCATGGACGTGTCATGGCTAACGGAAACACATGTTGTTACTTCATT 324					RESULT 1.2	
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						DEFINITION Q3A2002.yg_ab1.QG_ABCDI	603 bp mRNA linear
							Q3A20020, mRNA sequence.
							Lactuca sativa cDNA clone

ACCESSION VERSION	B0847005	EST.	RESULT 13
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SOURCE	Lactuca sativa		
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytina; Magnoliophyta; euicotyledons; core eudicots; asterids; campanulids; Asterales; Asteraceae; Cichorioideae; Chlorieae; Lactuca.	LOCUS	AU306450
REFERENCE	1. (bases 1 to 603)	DEFINITION	447 bp mRNA linear EST 22-JAN-2004 zinnia cultured mesophyll cell equalized cDNA Zinnia elegans cDNA clone 216034, mRNA sequence.
AUTHORS	Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L., Lirn,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegler,J., Lai,Z., Church,S., Jackson,L. and Bradford,K.	ACCESSION VERSION	AU306450
TITLE	Lettuce and Sunflower ESTs from the Composite Genome Project	KEYWORDS	AU306450 1 GI:41122386 EST.
JOURNAL	Unpublished (2002)	ORGANISM	Zinnia elegans
COMMENT	Contact: Alexander Kozik [R.W.Michelmore] Department of Vegetable Crops, R.W.Michelmore Lab University of California at Davis (UCD) Arimondson Hall, UCD, Davis, CA 95616, USA Tel.: 1-(530)-752-1742 Fax: 1-(530)-752-9659 Email: akozik@atgc.org [michelmore@vegmaill.ucdavis.edu] belongs to contig QG_CA_Contig9686, see <a href="http://cgdb.ucdavis.edu/">http://cgdb.ucdavis.edu/</a> for details.	REFERENCE	Demura,T., Tashiro,G., Kishimoto,N., Kubo,M., Matsuo,N., Minami,A., Nagata-Hiwashi,M., Nakamura,K., Okamura,Y., Sasaki,N., Suzuki,S., Yazaki,J., Kikuchi,S. and Fukuda,H.
FEATURES	Plate: QGA20 row: O column: 20.	ORGANISM	Zinnia elegans
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source	1.	/db_xref="taxon:4236"	/db_xref="eaxon:34245"
source	1	/clone="QGA20020"	/clone="Z16034"
source	1	/lab_host="E.coli"	/tissue type="mesophyll cell"
source	1	/clone lib="QG_ABCDI lettuce salinas"	/clone lib="zinnia cultured mesophyll cell equalized cDNA"
source	1	/note="Vector: pBRCDNA3.1B; The library was constructed from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made into four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at <a href="http://cgdb.ucdavis.edu/">http://cgdb.ucdavis.edu/</a> TAG_TISSUE=germinating seeds TAG_LIB=QG_ABCDI lettuce salinas TAG_SEQ=TCCTGCGGG"	/note="Vector: pGEM-T easy; cultured in tracheary element differentiation-inductive medium"
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		DB	1;
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		Matches	160;
		Best Local Similarity	77.7%;
		Score	122;
		DB	1;
		Length	447;
		Pred. No.	4-22;
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		Conservative	45;
		Matches	160;
		Best Local Similarity	77.7%;
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